

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 05:02:30 ; Search time 1535.21 Seconds
(without alignments)
1170.088 Million cell updates/sec

Title: US-08-790-540A-1

Perfect score: 351

Sequence: 1 CAGGTGCAGCTGCTGGAGTC.....CTACAGTGAAGTCTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_bal.*

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6: gb_pli.*

7: gb_pl2.*

8: gb_pr1.*

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11: gb_ro.*

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13: gb_un.*

14: em_fun.*

15: em_hum1.*

16: em_hum2.*

17: em_in.*

18: em_om.*

19: em_or.*

20: em_ov.*

21: em_pat.*

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23: em_pl.*

24: em_ro.*

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70: gb_htg23.*
71: gb_vil.*
72: gb_vil2.*
73: gb_ba3.*
74: em_htg8.*
75: em_htg9.*
76: em_htg10.*
77: gb_pr6.*
78: gb_pr7.*
79: gb_sts1.*
80: gb_sts2.*
81: gb_pat1.*
82: gb_pat2.*
83: em_htg0.*
84: gb_htg24.*
85: gb_pr8.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	268.6	76.5	482	81	I08289	I08289 Sequence 6
2	268.6	76.5	488	11	S45356	S45356 Immunoglob
3	258.8	73.7	354	11	MUSIGMUD2A	M83724 Mouse monoc
4	257.4	73.3	413	81	A38870	A38870 Sequence 24
5	257.4	73.3	413	81	AR013776	AR013776 Sequence
6	257.4	73.3	721	81	AR027762	AR027762 Sequence
7	257.4	73.3	721	81	AR088763	AR088763 Sequence
8	257.4	73.3	733	81	AR027763	AR027763 Sequence
9	257.4	73.3	733	81	AR088764	AR088764 Sequence
10	254.8	72.6	348	11	MUSIGHVAB	L09000 Mus musculu
11	254.8	72.6	351	11	MUSIGHVACV	M34737 Mouse Ig H-
12	254.4	72.5	414	11	MMU62048	U62048 Mus musculu
13	254	72.4	354	11	AF113106	AF113106 Mus muscu
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15	254	72.4	354	11	AF113108	AF113108 Mus muscu
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17	251.8	71.7	598	11	S55737	S55737 VH-immunogl
18	251	71.5	351	21	E09589	E09589 cDNA encodi
19	250.2	71.3	637	11	S79401	S79401 VH183-DSP2
20	249.4	71.1	351	21	E09587	E09587 cDNA encodi
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25 246.8 70.3 351 11 MMU293331 Mus muscu
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27 246.2 70.1 351 11 MDSIGVAAU
28 246.2 70.1 480 11 MMRRK16V
29 246.2 70.1 1115 11 MMRRK16G
30 246 70.1 363 11 MDIGGVAH
31 245.8 70.0 346 11 MMU55542
32 245.4 69.9 744 12 SCO250759
33 245.2 69.9 351 11 AF098319
34 245.2 69.9 351 11 AF163750
35 245.2 69.9 384 11 U01089
36 244.8 69.7 393 11 MMU02306
37 244.8 69.7 418 11 S67234
38 244.8 69.7 418 81 AR022586
39 244.8 69.7 418 81 AR037601
40 244.8 69.7 764 11 M23627
41 244.4 69.6 729 5 AX011069
42 243.6 69.4 359 11 S71117
43 243.6 69.4 375 11 MMHCVR15
44 243.4 69.3 420 11 AF045520
45 243.2 69.3 720 11 MMU40582

ALIGNMENTS

RESULT 1
LOCUS I08289 482 bp PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0380068.
ACCESSION I08289
VERSION I08289.1 GI:589001
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 482)
AUTHORS Zerler,B.D.
TITLE An expression system for production of chimeric monoclonal antibodies
JOURNAL Patent: EP 0380068-A1 6 01-AUG-1990;
FEATURES Location/Qualifiers
source 1..482
BASE COUNT 112 a 116 c 130 g 124 t
ORIGIN

Query Match 76.5%; Score 268.6; DB 81; Length 482;
Best Local Similarity 85.9%; Pred. No. 4.5e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCCTGAGACTCT 61
DB 133 AAGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCCTGAGACTCT 192
QY 62 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 121
DB 193 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 252
QY 122 CGGCAAGGCTCTGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
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QY 182 TAGACACTGTGCAGGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 241
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Db 373 TGCAAATGAGCAGTCTGAAGTCTGAGGACACAGCCGCTGATTACTGTGCAAGAAGGTACG 432
QY 302 ACGCAGTTTGGCTTACTTGGGCAAGGACTACAGTCACTGTTTCT 348
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RESULT 2
LOCUS S45356 488 bp mRNA ROD 08-MAY-1993
DEFINITION immunoglobulin heavy chain variable-anti-human IL-2R [mice, mRNA
ACCESSION S45356
VERSION S45356.1 GI:255660
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 488)
AUTHORS Rose,B., Gillespie,A., Wunderlich,D., Kelley,K., Dzuiba,J.,
Shedd,D., Cahill,K. and Zerler,B.
TITLE Differential effects of a murine and chimeric mouse/human
anti-interleukin-2 receptor antibody on human T-cell proliferation
JOURNAL Immunology 76 (3), 452-459 (1992)
MEDLINE 92406249
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 115041] from the original journal article.
This sequence comes from Fig. 1b.
FEATURES Location/Qualifiers
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CDS .
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BASE COUNT 114 a 116 c 132 g 126 t
ORIGIN

Query Match 76.5%; Score 268.6; DB 11; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.5e-77;
Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCCTGAGACTCT 61
DB 138 AAGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCTGGAAGGTCCCTGAGACTCT 197
QY 62 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 121
DB 198 CCTGTGCAGCTCTGGATTCACCTTCAGTAGCTATGACATGCTTTGGGTTGCCAGGCTC 257
QY 122 CGGCAAGGCTCTGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTAGCACCCTACTATT 181
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QY 182 TAGACACTGTGCAGGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 241
DB 318 CAGACACTGTGAAGGCGGATTCACCTTCAGAGACAATAGTAGAACAACCCCTATACC 377
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Db 378 TGCAGTACGACCTCTGAAGTCTGAGGACACAGCCGCTGTATTACTGTGCAAGAGTAGC 437
QY 302 ACGGCACTTTTGTCTACTGGGCGCAAGGAGCTAGACGTGACTGTTCT 348
Db 438 GCCTCCCTTTTGTCTACTGGGCGCAAGGAGCTGTGTCACCTGCTCT 484

RESULT 3
LOCUS MUSIGMUD2A 354 bp mRNA ROD 08-MAY-2000
DEFINITION Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
ACCESSION M83724
VERSION M83724.1 GI:197951
KEYWORDS D-region; Ig heavy chain; J-region; V-region; Immunoglobulin;
immunoglobulin mu-chain; monoclonal antiidiotypic antibody.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS 1 (bases 1 to 354)
Taub, R., Hsu, J. C., Garsky, V. M., Hill, B. L., Erlanger, B. F. and
Kohn, L. D.
TITLE Peptide sequences from the hypervariable regions of two monoclonal
anti-idiotypic antibodies against the thyrotropin (TSH) receptor
are similar to TSH and inhibit TSH-increased cAMP production in
FRTL-5 thyroid cells
JOURNAL J. Biol. Chem. 267 (9), 5977-5984 (1992)
MEDLINE 92210565
FEATURES
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BASE COUNT 79 a 81 c 108 g 86 t
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 7.2e-74;
Matches 300; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTCTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
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Db 62 CCTGTGACGCTTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGCTC 121
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Db 122 CAGAGAAGGCTGGAGTGGTGCAGAAATAGTAGTGGTGGTGTAGTACACCTACTATC 181
QY 182 TAGACACTGTGACAGGCCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCTATACC 241
Db 244 TAGACAGTGTGAAGGCCGATTCCACCATCTCCAGAGACAGTGCAGAGAACACCTATACC 303
QY 242 TGCAGTGTGAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATACT 301
Db 304 TGCAGTGTGAGTCTCTGAGAGCGGAGGCTGTGAGGACACGCGCTTGTATTACTGTGCAAGCAGTACGG 363
QY 302 ACGGCACTTTTGTCTACTGGGCGCAAGGAGCTAGACGTGACTGTTCT 348
Db 364 TAGTCCCGTTTGTCTACTGGGCGCAAGGAGCTCTGGTCCACCGTCTCT 410

RESULT 5
LOCUS AR013776
DEFINITION Sequence 56 from patent US 5773001.
ACCESSION AR013776
VERSION AR013776.1 GI:3971230
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Db 182 CAGACACTGTGACGGCGCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCTATACC 241
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Db 242 TGCAGTGTGAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATACT 301
QY 299 ACTACGCGAGTCTTGTCTACTGGGCGCAAGGAGCTAGACGTGACTGTTCT 348
Db 302 ACTACGCGAGTCTTGTCTACTGGGCGCAAGGAGCTCTGGTCACTGTTCT 351

RESULT 4
LOCUS A38870
DEFINITION Sequence 24 from Patent WO9413805.
ACCESSION A38870
VERSION A38870.1 GI:2295288
KEYWORDS unidentifed.
SOURCE unidentifed.
ORGANISM unidentifed.
REFERENCE 1 (bases 1 to 413)
AUTHORS King, D. J., Aguirre, J. R. and Owens, R. J.
TITLE HUMANISED ANTIBODIES DIRECTED AGAINST A33 ANTIGEN
JOURNAL Patent: WO 9413805-A 24 23-JUN-1994;
CELLTECH LTD (GB)
COMMENT Other publication AU 5656894 940704
Other publication GB 2278357 941130
Other publication JP 7504334T 950518.
FEATURES
    Location/Qualifiers
        source
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BASE COUNT 88 a 99 c 118 g 108 t
ORIGIN

Query Match 73.3%; Score 257.4; DB 81; Length 413;
Best Local Similarity 83.9%; Pred. No. 2.1e-73;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
Db 64 AAGTGAAGCTGTGGAGTCTGGGGAGGCTTACTGAAGCCTGGAGGTCCTGAAACTCT 123
QY 62 CCTGTGACGCTCTGAGTTCACCTTCAGTAGCTATGACATGCTTGGGTTCGCCAGCTC 121
Db 124 CCTGTGACGCTCTGAGTTCGCTTTCAGTAGCTATGACATGCTTGGGTTCGCCAGCTC 183
QY 122 CGGGCAAGGCTCTGGAGTGGTGCAGAAAGTTAGTAGTGGTGGTGTAGCACCCTACTATT 181
Db 184 CGGAGAAGGCTGGAGTGGTGCAGAACCATTAGTAGTGGTGGTGTAGTACACCTACTATT 243
QY 182 TAGACACTGTGACAGGCCGATTCCACCATCTCCAGAGACAAATAGTAAGAACACCTATACC 241
Db 244 TAGACAGTGTGAAGGCCGATTCCACCATCTCCAGAGACAGTGCAGAGAACACCTATACC 303
QY 242 TGCAGTGTGAGTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATACT 301
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QY 302 ACGGCACTTTTGTCTACTGGGCGCAAGGAGCTAGACGTGACTGTTCT 348
Db 364 TAGTCCCGTTTGTCTACTGGGCGCAAGGAGCTCTGGTCCACCGTCTCT 410

RESULT 5
LOCUS AR013776
DEFINITION Sequence 56 from patent US 5773001.
ACCESSION AR013776
VERSION AR013776.1 GI:3971230
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KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 413)

TITLE Hamann,P.Ross, Hanman,L., Hollander,I., Holcomb,R., Hallett,W., Tsou,H. and Weiss,M.J.
Conjugates of methyltrithio antitumor agents and intermediates for their synthesis

JOURNAL Patent: US 5773001-A 56 30-JUN-1998;

FEATURES Location/Qualifiers

source i..413

BASE COUNT 88 a 100 c 117 g 108 t

ORIGIN /organism="unknown"

Query Match 73.3%; Score 257.4; DB 81; Length 413;

Best Local Similarity 83.9%; Pred. No. 2.1e-73;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGGTTGTGCAGCCTGGAAGGTCCTGAGACTCT 61

DB 64 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCTGGAGGTCCTGAAACTCT 123

QY 62 CCTGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGCTTGGGTTGCGAGGCTC 121

DB 124 CCTGTGCAGCCTCTGGATTGCGCTTCAGTACCTATGACATGCTTGGGTTGCGAGCTC 183

QY 122 CGGGCAAGGCTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCCTACTATT 181

DB 184 CGGAGAAGGCTGGAGTGGGTCGCAACCACTAGTAGTGGTGGTAGCTACTATT 243

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QY 302 AGGGCAGTTTCTGTTACTGGGCGCAAGGACTACAGTACTGTTTCT 348

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RESULT 6

AR027762

LOCUS AR027762 721 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 15 from patent US 5856456.

ACCESSION AR027762

VERSION AR027762.1 GI:5938582

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 721)

TITLE Whitlow,M.D. and Filpula,D.R.

LINKER Linker for linked fusion polypeptides

JOURNAL Patent: US 5856456-A 15 05-JAN-1999;

FEATURES Location/Qualifiers

source i..721

BASE COUNT 176 a 172 c 189 g 184 t

ORIGIN /organism="unknown"

Query Match

Best Local Similarity 73.3%; Score 257.4; DB 81; Length 721;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGGTTGTGCAGCCTGGAAGGTCCTGAGACTCT 61

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QY 62 CCTGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGCTTGGGTTGCGAGGCTC 121

DB 124 CCTGTGCAGCCTCTGGATTGCGCTTCAGTACCTATGACATGCTTGGGTTGCGAGCTC 183

QY 122 CGGGCAAGGCTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCCTACTATT 181

DB 184 CGGAGAAGGCTGGAGTGGGTCGCAACCACTAGTAGTGGTGGTAGCTACTATT 243

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QY 62 CCGTGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGCTTGGGTTGCGAGGCTC 121

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DB 545 TAGACAGTGTGAAGGCCGATTCACCATCTCCAGACACATAGTAGAAGACCCCTATACC 604

QY 242 TGCATAAGTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301

DB 605 TGCATAAGTCTCTGAGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 664

QY 302 ACGGCGAGTTTCTGTTACTGGGCGCAAGGACTACAGTACTGTTTCT 348

DB 665 TAGTCCCGTTTCTTACTGGGCGCAAGGACTCTGGTCACTGCTCTCT 711

RESULT 7

AR088763

LOCUS AR088763 721 bp DNA PAT 07-SEP-2000

DEFINITION Sequence 15 from patent US 5990275.

ACCESSION AR088763

VERSION AR088763.1 GI:10015526

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 721)

AUTHORS Whitlow,M.D. and Filpula,D.R.

TITLE Linker and linked fusion polypeptides

JOURNAL Patent: US 5990275-A 15 23-NOV-1999;

FEATURES Location/Qualifiers

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BASE COUNT 176 a 172 c 189 g 184 t

ORIGIN /organism="unknown"

Query Match 73.3%; Score 257.4; DB 81; Length 721;

Best Local Similarity 83.9%; Pred. No. 2.2e-73;

Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGGTTGTGCAGCCTGGAAGGTCCTGAGACTCT 61

DB 365 AAGTGAAGCTGTGGAGTCTGGGGAGCGCTTAGTGAAGCCTGGAGGTCCTGAAACTCT 424

QY 62 CCGTGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGCTTGGGTTGCGAGGCTC 121

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Db	497	CGGAGAAGAGCGCTGGAGTGGGTGCGAACCACTTAGTGGTGGTGGTAGCTACTATT	556	I	I	I	I	I	I
QY	182	TAGACACTGTGCAGGCGCCGATTACCACATCTCCAGAGACAATAGTAAACAACCCCTATACC	241	I	I	I	I	I	I
Db	557	TAGACACTGTGCAGGCGCCGATTACCACATCTCCAGAGACAGTGCAGGAGAACCCTATACC	616	I	I	I	I	I	I
QY	242	TGCAATGAARACTCTGTAGAGCCGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT	301	I	I	I	I	I	I
Db	617	TGCAATGAGCAGCTCTGAGCTCTGAGGACACGGCCTTGTTACTGTGCACCGACTACGG	676	I	I	I	I	I	I
QY	302	ACGCAGTTTTGCTTACTGGGCGCAAGGACTACAGTGACTGTTTCT	348	I	I	I	I	I	I
Db	677	TAGTCCGTTTGTCTTACTGGGCGCAAGGACTCTGGTCACTGCTCT	723	I	I	I	I	I	I
RESULT	10								
MUSIGVAB									
LOCUS		MUSIGVABE	348 bp	mRNA	ROD			27-APR-1993	
DEFINITION		Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region							
ACCESSION		L09000							
VERSION		L09000.1	GI:197998						
KEYWORDS		V-region; Immunoglobulin V region; processed gene:							
SOURCE		Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.							
ORGANISM		Mus musculus							
REFERENCE		Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS		1 (bases 1 to 348)							
		Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,							
		Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.							
TITLE		V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr mice							
JOURNAL		J. Immunol.	150,	1591-1610	(1993)				
MEDLINE		93163585							
FEATURES		Location/Qualifiers							
source		'1..348							
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		/strain="mrl/mp-lpr/lpr"							
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		/cell_type="B-cell"							
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Query Match									
Best Local Similarity			72.6%;	Score 254.8;	DB 11;	Length 348;			
Matches	289;	Conservative	0;	Mismatches	57;	Indels	0;	Gaps	0;
QY	2	AGGTGCAGCTGGTGGAGCTCGGGGAGGCCGTTGTGCAGCCTGGAAGGTCCTGAGACTCT	61	I	I	I	I	I	I
Db	2	AAGTGAAGCTTGTGGAGCTCGGGGAGGCTTAGTGAAGCCCTGGAGGTCCTGAACTCT	61	I	I	I	I	I	I
QY	62	CCTGTGCAGCCTCTGGATTACACCTTCAGTAGCATATGACATGTCTTGTTGGTTGCCAGGCTC	121	I	I	I	I	I	I
Db	62	CCTGTGCAGCCTCTGGATTACATTTTCAGTAGCATATACCATGTCTTGTTGGTTGCCAGACTC	121	I	I	I	I	I	I
QY	122	CGGCAAGGCTCTGGAGTGGGTGCGAANAAGTTAGTAGTGGTGGTGGTAGCACCTACTATT	181	I	I	I	I	I	I

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Db 122 CGCGAAGAGCTGGAGTGGGTCGTACCACTAGTAGTGGTGGTAGCACTACTATC 181
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCTATACC 241
Db 182 CAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATGCCAGAACACCTGTACC 241
QY 242 TGCAATGAATCTCTCTGAGAGCCGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 242 TGCAATGACAGCTCTGAGTCTCAGGACACAGCGCCATGTATTACTGTGCAAGAGGTT 301
QY 302 ACGCCAGTTTGTCTACTGGGCGCAAGGACTACAGTACTGTTC 347
Db 302 ACTCCCTATGACTACTGGGCTCAAGGAACCTCAGTCAAGCTC 347

RESULT 11
LOCUS MUSIGHACV 351 bp mRNA ROD 27-APR-1993
DEFINITION Mouse Ig H-chain mRNA VDJ-region, partial cds.
ACCESSION M34737
VERSION M34737.1 GI:194750
KEYWORDS V-region; J-region; V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain BALB/c) adult spleen anti-HA hybridoma H35-D1, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 351)
AUTHORS Clarke,S.H., Staudt,L.M., Kavalier,J., Schwartz,D., Gerhard,W.U. and Weigert,M.G.
TITLE V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin
JOURNAL J..Immunol. 144, 2795-2801 (1990)
MEDLINE 90203619
FEATURES
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BASE COUNT      89 a  82 c  99 g  81 t
ORIGIN

Query Match      72.68; Score 254.8; DB 11; Length 351;
Best Local Similarity 83.5%; Pred. No. 1.5e-72;
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QY 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTGACGCTGGAAGTCCCTGAGACTCT 61
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Db 62 CCTGTGAGCCTCTGGATTACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121
QY 122 CGGCAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGGTGGTGGTGGTGGTGGTGGT 181
Db 122 CGGAAAAGAGGCTGGAGTGGTCCAAACCAATTAGTAGTGGTGGTGGTGGTGGTGGT 181
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCTATACC 241
Db 182 CAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATGCCAGAACACCTGTACC 241
QY 242 TGCAATGAATCTCTCTGAGAGCCGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 242 TGCAATGACAGCTCTGAGTCTCAGGACACAGCGCCATGTATTACTGTGCAAGAGGTT 301
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Db 242 TGCAATGACAGCTCTGAACTCTGAGGACACAGCCATGTATTACTGTGCAAGTATTACT 301
QY 302 ACGCCAGTTTGTCTACTGGGCGCAAGGACTACAGTACTGTTC 347
Db 302 ACGTAGGATTGACTACTGGGCGCAAGGACCACTCTCAGAGTCTC 347

RESULT 12
LOCUS MMU62048 414 bp mRNA ROD 19-FEB-1997
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin IgM heavy chain mRNA, partial cds.
ACCESSION U62048
VERSION U62048.1 GI:1438576
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and Dighiero,G.
TITLE Structural and affinity studies of IgM polyreactive natural autoantibodies
JOURNAL J. Immunol. 158 (2), 968-976 (1997)
MEDLINE 97146071
REFERENCE 2 (bases 1 to 414)
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and Dighiero,G.
TITLE Direct Submision
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France
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    /organism="Mus musculus"
    /strain="(CBA/NxBALB/c)F1"
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    /sex="female"
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BASE COUNT      88 a  110 c  115 g  101 t
ORIGIN

Query Match      72.5%; Score 254.4; DB 11; Length 414;
Best Local Similarity 84.6%; Pred. No. 2e-72;
Matches 301; Conservative 0; Mismatches 46; Indels 9; Gaps 1;

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QY 62 CCTGTGAGCCTCTGGATTACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121
Db 62 CCTGTGAGCCTCTGGATTACCTTCAGTATGATGATGATGATGATGATGATGATGAT 121
QY 122 CGGCAAGGCTCTGGAGTGGTCCAAAGTTAGTAGTGGTGGTGGTGGTGGTGGTGGT 181
Db 122 CGGAGAGAGGCTGGAGTGGTCCCAACCAATTAGTAGTGGTGGTGGTGGTGGTGGT 181
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATAGTAAGAACACCTATACC 241
Db 182 CAGACAGTGTGAAGGCGCGATTACCATCTCCAGAGACAATGCCAGAACACCTGTACC 241
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Qy	302	ACGG--	--CAC	TTTTGCTTACTGGGCGCAAGGACTACAGTCACG	TTTCT	348
Db	302	ATAGTA	ACTCTTTGCTTACTGGGCGCAAGGACTCTGGTCAC	TGCTCT	351	
RESULT	14					
AF113107						
LOCUS	AF113107	354 bp	nrna	ROD	21-SEP-2000	
DEFINITION	Mus musculus hybridoma Y6-8G3 anti-myeloperoxidase immunoglobulin heavy chain variable region mRNA, partial cds.					
ACCESSION	AF113107					
VERSION	AF113107.1					
KEYWORDS	GI:4768654					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 354)					
AUTHORS	Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J., Jennette,J.C. and Nachman,P.H.					
TITLE	Restriction in V kappa gene use and antigen selection in anti-myeloperoxidase response in mice					
JOURNAL	J. Immunol. 165, 3890-3897 (2000)					
REFERENCE	2 (bases 1 to 354)					
AUTHORS	Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., Kinjoh,K., Tuttle,R. and Taylor,J.					
TITLE	Direct Submission					
JOURNAL	Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525, Chapel Hill, NC 27599, USA					
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CDS						
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ORIGIN	g 88 t					

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QY	62	CCTGTGCAGCCTCTGGATTCACTTTCAGTATGACATGTCTTTGGTTCGCCAGGCTC	121	
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QY	122	CGGCAAGGTCGTGGAGTGGTGCAGAAAGTTAGTGTGGTGGTAGCACCCTACTATT	181	
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QY	182	TAGACACTGTGCAGGGCCGATTCCACTCTCCAGAGACAATAGTAGAACACACCCTATACC	241	
DB	182	CAGACAGTGTGAAGGGTCGATTCACTCTCCAGAGACAATGCCAAGAACAACTGTACC	241	

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QY 302 ACGG---CAGTTTTCCTTACTGGGCCCAAGGACACAGTACTGTTTCT 348
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RESULT 15
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LOCUS Mus musculus hybridoma Y6-9G3 anti-myeloperoxidase immunoglobulin
DEFINITION heavy chain variable region mRNA, partial cds.
ACCESSION AF113108
VERSION AF113108.1 GI:4768656
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Jethwa,H.S., Clarke,S.H., Itoh-Lindstrom,Y., Falk,R.J.,
Jennette,J.C. and Nachman,P.H.
TITLE Restriction in V kappa gene use and antigen selection in
anti-myeloperoxidase response in mice
J. Immunol. 165: 3890-3897 (2000)
JOURNAL anti-myeloperoxidase response in mice
AUTHORS 2 (bases 1 to 354)
Jethwa,H.S., Nachman,P.H., Jennette,J.C., Falk,R.J., KinJoh,K.,
Tuttle,R. and Taylor,J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1998) Pathology, UNC Chapel Hill, CB# 7525,
Chapel Hill, NC 27599, USA
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ORIGIN
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Query Match 72.4%; Score 254; DB 11; Length 354;
Best Local Similarity 84.9%; Pred. No. 2.7e-72;
Matches 297; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
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QY 62 CCGTGACAGCTCTGAGTTCACCTTCAGTAGCTATGATGCTTGGGTTCGCCAGGCTC 121
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QY 122 CGGCAAGGCTTGGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTAGCCACTACTATT 181
||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 |||||
Db 122 CGGCAAGGCTTGGAGTGGGTTCGCAAAAGTTAGTAGTGGTGGTAGCCACTACTATT 181
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QY 182 TAGACACTGTGCAGGCGCGATCCACTCTCCAGAGACAANTAGTAAGAACCCCTATACC 241
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QY 242 TGCAATGAAGTCTCTGAGAGCCGAGGACACAGCCGTTATTACTGTGCAAGACATAACT 301
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Db 242 TGCAATGAGCAGTCTGAGGCTGAGGACACAGCCCTTATTACTGTGCAAGAGGTTACT 301
||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 |||||

QY 302 ACGG---CAGTTTTCCTTACTGGGCCCAAGGACACAGTACTGTTTCT 348
||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 |||||
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 01:33:05 ; Search time 1450.07 Seconds
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Perfect score: 351
Sequence: 1 CAGGTCAGTGTGTGAGTC.....CTACAGTACTGTTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230.4	65.6	469	23	AI645111 ms87g10.y
2	230.4	65.6	823	3	AA170256 ms87g10.y
3	229.8	65.3	406	90	AW401971 UI-HF-BKO
4	228.4	65.1	454	95	AW824857 us08c01.y
5	226.8	64.6	440	90	AW408304 UI-HF-BKO
6	226.6	64.4	511	90	AW402613 UI-HF-BKO
7	224.6	64.0	548	90	AW408295 UI-HF-BKO
8	223.8	63.9	436	90	AW402311 UI-HF-BKO
9	223.4	63.6	456	90	AW403059 UI-HF-BKO
10	218.8	62.3	412	90	AW402895 UI-HF-BKO
11	218.2	62.2	487	90	AW403862 UI-HF-BKO
12	217.8	62.1	471	90	AW403220 UI-HF-BKO
13	217.6	62.0	483	90	AW403901 UI-HF-BKO
14	217.2	61.8	491	90	AW402907 UI-HF-BKO
15	216.2	61.5	518	90	AW402029 UI-HF-BKO
16	215.6	61.5	390	93	AW631411 hh85d05.y
17	215.6	61.4	361	90	AW403412 UI-HF-BKO
18	215.4	61.4	536	90	AW402624 UI-HF-BKO
19	214.8	61.2	447	90	AW402793 UI-HF-BKO
20	214.6	61.1	372	9	AA581192 nd38b11.r
21	214.6	61.1	582	90	AW401386 UI-HF-BKO
22	214.6	61.0	503	90	AW402572 UI-HF-BKO
23	214.6	61.0	516	90	AW401728 UI-HF-BKO
24	213.8	60.9	406	90	AW403983 UI-HF-BKO
25	213.6	60.9	397	90	AW403886 UI-HF-BKO
26	211.6	60.3	475	90	AW402740 UI-HF-BKO
27	211.2	60.2	510	90	AW403707 UI-HF-BKO
28	210.6	60.0	396	90	AW407843 UI-HF-BKO
29	209.9	59.5	413	90	AW402865 UI-HF-BKO
30	208.2	59.3	411	90	AW403298 UI-HF-BKO
31	207.8	59.2	484	90	AW401679 UI-HF-BKO
32	207.6	59.1	553	90	AW401769 UI-HF-BKO
33	206.6	58.9	443	90	AW401428 UI-HF-BKO
34	206.4	58.8	445	90	AW408316 UI-HF-BKO
35	206.4	58.7	511	90	AW402453 UI-HF-BKO
36	205.8	58.6	378	11	AA740786 OD32611.s
37	205.8	58.6	669	158	AQ472659 CITBI-E1-
38	205.6	58.6	459	90	AW402542 UI-HF-BKO
39	205.4	58.5	434	93	AW630702 hh86d11.y
40	204.8	58.3	677	106	BE286624 601090210
41	204.6	58.3	367	90	AW408326 UI-HF-BKO
42	204.4	58.2	405	90	AW402449 UI-HF-BKO
43	203.4	57.9	447	90	AW403163 UI-HF-BKO
44	203.4	57.8	412	95	AW800162 MR2-UM006
45	202.4	57.7	331	90	AW402553 UI-HF-BKO

ALIGNMENTS

RESULT 1
AI645111
LOCUS ms87g10.y1 Soares mouse 3nbms Mus musculus cDNA clone IMAGE:618594
DEFINITION 5' similar to gb:U23089 Mus musculus C17 SCID immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.
ACCESSION AI645111
VERSION AI645111.1 GI:4723586

EST 15-MAR-2000
ms87g10.y1 Soares mouse 3nbms Mus musculus cDNA clone IMAGE:618594
5' similar to gb:U23089 Mus musculus C17 SCID immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.

[illegible]

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Db 179 CCTGTGCAGCCCTCTGGATTCACTTTTCAGTAGCTATGCCATGCTCTGGGTTCCGCCAGACTC 238
Qy 122 CGGCAAGGGTCTGAGTGGGTCGAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181
Db 239 CAGAGAAGAGGCTGGAGTGGGTCGATACATAGTAGTGGTGGTATTACATCTTACTATG 298
Qy 182 TAGACACTGTGAGGCGCCATCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 299 CAGACACTGTGAAGGCGGATTCACCATCTCCAGAGACAATGCCAGGACACCCCTGTACC 358
Qy 242 TCGAAATGAACCTCTCTGAGAGCGGAGGACACAGCCGCTGATTACTGTGCAAGACAT 297
Db 359 TCGAAATGAGCAGTCTGAAGTCTGAGGACACAGCCATGATTACTGTACAAGAGAT 414

RESULT 3
AW401971 406 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BK0-aa0-C-04-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054342 5', mRNA sequence.
ACCESSION AW401971
VERSION AW401971.1 GI:6920657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
Source
1. 406
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054342"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb), directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 89 a 93 c 123 g 100 t
ORIGIN
Query Match 65.5%; Score 229.8; DB 90; Length 406;
Best/Local Similarity 80.9%; Pred.No. 2.4e-59;
Matches 280; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

Qy 2 AGGTGCAGCTGTGGAGTCTGGGGAGCGGTGTGCAGCCTGGAAAGGTCCTCGAGACTCT 61
Db 60 AGGTGCAGCTGTGGAGTCTGGGGAGCGTGTGTACAGCCTGGAGGTCCTCGAGACTCT 119
Qy 62 CCTGTGCAGCCCTCTGGATTCACCTTCAGTAGCTATGCCATGCTCTGGGTTCCGCCAGGCTC 121
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Db 120 CCTGTGCAGCCTCTGGATTCACTTCAGTAGTATGAATGAAGTGGTCCGCCAGGCTC 179
Qy 122 CGGCAAGGGTCTGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCAGCTACTATT 181
Db 180 CAGGAAGGGGCTGGAGTGGGTTTCATACATAGTAGTAGTGGTAGTACCATATACTACG 239
Qy 182 TAGACACTGTGAGGCGGATTCACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241
Db 240 CAGACTCTGTGAAGGCGGATTCACCATCTCCAGAGACAACGCCNAGAACCTACTGTATC 299
Qy 242 TCGAAATGAATCTCTCTGAGAGCCGAGGACACAGCGGCTGATTACTGTGCAGACATAC 301
Db 300 TCGAAATGAACAGCTGAGAGCCGAGGACACGCTGTTTATTACTGTGCGAGTCAATATA 359
Qy 302 ACGCAGCTTTGCTTACTTGGGCGCAAGGACTACAGTCTGACTGTTTC 347
Db 360 ACAACAGCT---GGTACTGGGCGCAGGGAACCCCTGGTCACCCGCTCTC 402

RESULT 4
AW824857 454 bp mRNA EST 17-MAY-2000
LOCUS us08c01.y1 Soares_NMGBC_B-cell Mus musculus cDNA clone
DEFINITION IMAGE:3136464 5' similar to gb:U14584 IG HEAVY CHAIN PRECURSOR
V-III REGION (HUMAN); gb:U23089 Mus musculus CB17 SCID
immunoglobulin heavy chain V region mRNA, (MOUSE);, mRNA sequence.
ACCESSION AW824857
VERSION AW824857.1 GI:7917934
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 454)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1061924
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 454
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3136464"
/clone_lib="Soares_NMGBC_B-cell"
/tissue_type="germinal B-cell from resting spleen"
/lab_host="DH10B (phage resistant)"
/notes="vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCAGGATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 102 a 109 c 127 g 116 t
ORIGIN
Query Match 65.1%; Score 228.4; DB 95; Length 454;
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Query Match          64.6%; Score 226.8; DB 90; Length 440;
Best Local Similarity 82.1%; Pred. No. 2e-58;
Matches 261; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY	2	AGGTGCAGCTGGTGGAGCTCGGGGAGCGGTGTGCAGCCTGGAAGGTCCCTGAGACTCT	61
Db	120	AGGTGCAGCTGGTGGAGCTCGGGGAGCGTGTGTACACCTGGAGGGTCCCTGAGACTCT	179
QY	62	CTGTGCAGCTCTGTGGANTCACCTTCAGTACGTATGACATGTCTTGGTTCGCCAGGCTC	121
Db	180	CTGTGCAGCCTCTGGATTTCACCTTCAGTAGTTATGAAATGGAACCTGGTCCGCCAGGCTC	239
QY	122	CGGGCAAGGCTCTGGAGTGGGTGCGAAAGTTAGTATGTTGGTGGTAGCACCTTACTATT	181
Db	240	CAGGGAAGGGCGTGGAGTGGGTTTCATACATTAGTAGTGGTAGTACCATATACACTACG	299
QY	182	TAGACACTGTGCAGGGCGGATTCCACATCTCCAGAGACAATAGTAGAACACACCCCTATACC	241
Db	300	CAGACTCTGTGAAGGGCGGATTCCACATCTCCAGAGACAACGCCAAGAAGCTCACTGTATC	359
QY	242	TGCAAAATGAACTCTCTCAGAGCCGAGACACAGCCGTGTATTACTGTGCGAGAGCATAACT	301
Db	360	TGCAAAATGAAACAGCCTGAGAGCCGAGACACAGCGCTGTTTATTACTGTGCGAGAGGGCA	419

Db	420	GCAGCTGGTCCCTTGACT	437
RESULT	6		
AW402613			
LOCUS	AW402613	511 bp	mrna
DEFINITION	UI-HF-BK0-aax-g-03-0-UI.r1	EST	16-FEB-2000
	IMAGE:3055305	5', mRNA sequence.	
ACCESSION	AW402613		
VERSION	AW402613.1	GI:6921317	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 511)		
AUTHORS	NIH-MGC	http://www.ncbi.nlm.nih.gov/MGC/.	

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be

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clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..511
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3055305"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (JT1)"
/notes="vector: pT773-Pac; Site1: NotI; Site2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt. Ph.D. Library preparation by Maria de Fatima

```

Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt. Ph.D. library preparation by Maria d'Eustachio.

/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 89 a 109 c 136 g 102 t
ORIGIN

Query Match 63.8%; Score 223.8; DB 90; Length 436;
Best Local Similarity 79.3%; Pred. No. 1.6e-57;
Matches 280; Conservative 0; Mismatches 67; Indels 6; Gaps 1;
QY 1 CAGGTGACGCTGGTGGAGCTGGGGAGCGCTGTGTGCACCTGGAGGTCCTCGAGACTC 60
DB 71 CAGGTGCAACTGGTGGAGCTGGGGAGCGGTGTGCCACCTGGAGGTCCTCGAGACTC 130
QY 61 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCT 120
DB 131 TCCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCT 190
QY 121 CCGGCAAGGCTCTGGAGTGGGTGCCAAGTAGTAGTGGTGGTAGCCTACTAT 180
DB 191 CCGGCAAGGCTCTGGAGTGGGTGCCAAGTAGTAGTGGTGGTAGCCTACTAT 250
QY 181 TTAGACACTGTCCAGGCGGATTCCACCTCTCCAGAGCAATAGTAAGAACCCCTATAC 240
DB 251 GCAAACTCGTGAAGGCGGATTCCACCTCTCCAGAGCAATAGTAAGAACCCCTATAC 310
QY 241 CTGCAAACTGCTCTGAGAGCGGAGGACAGCGGCTGTATTACTGTGTCAGAGA ----- 294
DB 311 CTGCAATGAACTCTGAGAGCGGAGGACAGCGGCTGTATTACTGTGTCAGAGGAGCT 370
QY 295 CATACACTAGGAGCTTCTTCTACTGGGCGCAAGGACTACAGTACTGTTTC 347
DB 371 GGGACCTGGGCGCACTTTGACTACTGGGCGCAGGAAACCTGCTCACCGCTC 423

RESULT 9
AW403059 456 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BKO-aal-f-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054090 5', mRNA sequence.
ACCESSION AW403059
VERSION AW403059.1 GI:6921885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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1. 456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054090"

/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 103 a 104 c 139 g 110 t
ORIGIN

Query Match 63.6%; Score 223.4; DB 90; Length 456;
Best Local Similarity 84.5%; Pred. No. 2.2e-57;
Matches 251; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 2 AGGTGCACCTGGTGGAGTCTGGGGAGCGGTGTGCACCTGGAGGTCCTCGAGACTCT 61
DB 110 AGGTGCACCTGGTGGAGTCTGGGGAGCGCTGTGTGCACCTGGAGGTCCTCGAGACTCT 169
QY 62 CCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCTC 121
DB 170 CCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATCTCTGGGTTCCGCCAGGCTC 229
QY 122 CGGCAAGGCTCTGGAGTGGGTGCCAAGTAGTAGTGGTGGTAGCCTACTATT 181
DB 230 CAGGGAAGGCTCTGGAGTGGGTTCATACATTAGTAGTGGTAGCCTACTATT 289
QY 182 TAGACACTGTGCGAGGCGGATTCCACCTCTCCAGAGCAATAGTAAGAACCCCTATACC 241
DB 290 CAGACTCTGTGAAGGCGGATTCCACCTCTCCAGAGCAAGCCCAAGCACTGTATC 349
QY 242 TSCAACTCACTCTGAGAGCGGAGGACAGCGGCTATTACTGTCCAGACATA 298
DB 350 TGCAATGAGAGCGCTGAGAGCGGAGGACGCGCTTTATTACTGTGCGGACATA 406

RESULT 10
AW402895 412 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BKO-aaw-d-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3055170 5', mRNA sequence.
ACCESSION AW402895
VERSION AW402895.1 GI:6921669
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
1. 412
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3055170"
/clone_lib="NIH_MGC_36"


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/clone="IMAGE:3055710"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
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/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      98 a 127 c 143 g 103 t
ORIGIN

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Query Match      62.1%; Score 217.8; DB 90; Length 471;
Best Local Similarity 84.0%; Pred. No. 1.1e-55;
Matches 246; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY  2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGGTCCTTGAGACTCT 61
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Db  77 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTCAAGCCTGGGGGTCCTTGAGACTCT 136
    |||||
QY  52 CTTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGATGCTCTTGGGTTCGCCAGGCTC 121
    |||||
Db  137 CTTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGATGCTCTTGGGTTCGCCAGGCTC 196
    |||||
QY  122 CGGGCAAGGCTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCCTTACTATT 181
    |||||
Db  197 CAGGGAAGGGCTGGAGTGGGTCCTCATCCATTAGTAGTAGTGGTTCATATCTAGG 256
    |||||
QY  182 TAGACATGTGTCAGGCGCGGATTCACCATCTCCAGAGACAATAGTAAGAACACCTTATACC 241
    |||||
Db  257 CAGACTGAGTGAAGGCGGATTCACCATCTCCAGAGACAATAGTAAGAACACCTTATACC 316
    |||||
QY  242 TCCAAATGAACCTCTGAGAGCGGAGGACACAGCGGTGTTACTTGTGCAAGA 294
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Db  317 TCCAAATGAACCTCTGAGAGCGGAGGACACAGCGGTGTTACTTGTGCGAGA 369
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RESULT 13
AW403901
LOCUS      AW403901      483 bp      mRNA      EST      16-FEB-2000
DEFINITION UI-HF-BKO-abn-d-01-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056689 5', mRNA sequence.
ACCESSION  AW403901
VERSION     AW403901.1 GI:6922864
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 483)
AUTHORS     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert_Strausberg@nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.lnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

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FEATURES             Location/Qualifiers
     source            1..483
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3056689"

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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      104 a 107 c 152 g 120 t
ORIGIN

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Query Match      62.0%; Score 217.6; DB 90; Length 483;
Best Local Similarity 83.4%; Pred. No. 1.3e-55;
Matches 247; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY  2 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCAGCCTGGAAGGTCCTTGAGACTCT 61
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Db  128 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTACAGCGGGGGTCCCTTGAGACTCT 187
    |||||
QY  62 CTTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGATGCTCTTGGGTTCGCCAGGCTC 121
    |||||
Db  188 CTTGTGAGCCTCTGGATTCACCTTCAGTAGCTATGATGCTCTTGGGTTCGCCAGGCTC 247
    |||||
QY  122 CGGGCAAGGCTCTGGAGTGGGTCGCAAAAGTTAGTAGTGGTGGTAGCCTTACTATT 181
    |||||
Db  248 CAGGGAAGGGCTGGAGTGGGTCGCACTTATTATAGCGGTGGTAGTAGCAGACTATG 307
    |||||
QY  182 TAGACATGTGTCAGGCGCGGATTCACCATCTCCAGAGACAATAGTAAGAACACCTTATACC 241
    |||||
Db  308 CAGACTGCTGAAGGCGCGGTTCCACATCTCCAGAGACAATATCCAAAGAACGCTGTATC 367
    |||||
QY  242 TCCAAATGAACCTCTGAGAGCGGAGGACACAGCGGTGTTACTTGTGCAAGACAT 297
    |||||
Db  368 TCCAAATGAACCTCTGAGAGCGGAGGACACAGCGGTGTTACTTGTGCGATAGAT 423
    |||||

```

```

RESULT 14
AW402907
LOCUS      AW402907      491 bp      mRNA      EST      16-FEB-2000
DEFINITION UI-HF-BKO-aaw-e-12-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055222 5', mRNA sequence.
ACCESSION  AW402907
VERSION     AW402907.1 GI:6921686
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 491)
AUTHORS     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert_Strausberg@nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.lnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

```

```

FEATURES             Location/Qualifiers
     source            1..491
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055222"
                     /clone_lib="NIH_MGC_36"

```

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 08:23:45 ; Search time 103.87 Seconds
(without alignments)
1269.448 Million cell updates/sec

Title: US-08-790-540A-1

Perfect score: 351

Sequence: 1 CAGGTCAGCTGCTGGAGTC.....CTACAGTCACTGTTCTAGT 351

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

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1: /SID56/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SID56/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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4: /SID56/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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6: /SID56/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SID56/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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9: /SID56/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SID56/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SID56/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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14: /SID56/gcgdata/geneseq/geneseqn/NA1993.DAT:*
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16: /SID56/gcgdata/geneseq/geneseqn/NA1995.DAT:*
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21: /SID56/gcgdata/geneseq/geneseqn/NA2000.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	100.0	351	19 V49820	Vitaxin antibody h
2	302.2	86.1	351	19 V49822	LM609 antibody hea
3	268.6	76.5	482	11 Q05555	Sequence encoding
4	263.8	75.2	417	15 Q62804	Humanised murine K
5	263.8	75.2	417	16 Q87534	Humanised anti-KC-
6	259.6	74.0	582	18 T90020	DNA encoding heavy
7	259.6	74.0	761	20 X01214	Human antiFc epsil
8	259.6	74.0	770	20 X01216	Human antiFc epsil
9	257.4	73.3	413	15 Q68650	Mab A33 heavy chai
10	257.4	73.3	721	20 V99765	A33/212 single-cha
11	257.4	73.3	721	21 Z37397	Linked fusion prot
12	257.4	73.3	733	20 V99766	A33/218 single-cha

13	257.4	73.3	733	21	Z37398	Linked fusion prot
14	255	72.6	1938	19	V58929	A33 chimeric recep
15	252.4	71.9	411	19	V24243	Chimeric antibody
16	252.4	71.9	411	20	X00116	Human antibody hea
17	252.4	71.9	411	21	Z58914	DNA seq ID No: 58
18	251	71.5	351	16	Q96284	Human IgE receptor
19	249.4	71.1	351	16	Q96282	Human IgE receptor
20	249.4	71.1	351	18	T90025	cDNA encoding heav
21	249.2	71.0	411	19	V24232	Chimeric antibody
22	249.2	71.0	411	20	X00092	Mouse humanised an
23	249.2	71.0	411	21	Z58913	Mouse antibody H c
24	247.4	70.5	369	19	V07642	anti-CD22 monoclon
25	246.8	70.3	1329	18	T61281	Humanised anti-L-s
26	246.2	70.1	480	13	Q20070	MRK16-H chain. Ch
27	244.8	69.7	418	15	Q62764	Murine KC-4 immuno
28	244.8	69.7	418	15	Q62789	Murine KC-4 immuno
29	244.4	69.6	722	21	Z28996	Anti-human CTLA-4
30	244.4	69.6	729	21	Z28997	Anti-murine CTLA-4
31	243.6	69.4	414	21	Z35243	Humanised anti-ver
32	242.2	69.0	324	13	Q20303	B cell hybridoma 1
33	241.4	68.8	357	15	Q66409	VH coding region o
34	240.6	68.5	360	19	V04636	Chimeric humanised
35	240.6	68.5	720	19	V04638	Chimeric humanised
36	240.2	68.4	354	18	T43417	Xenograft antibody
37	240	68.4	441	18	T72269	Chimeric MAB 15 PC
38	239.8	68.3	357	19	V44997	15D3 antibody heav
39	239.8	68.3	357	20	Z10957	15D3 VH chain codi
40	239.8	68.3	357	20	V08933	Antibody 15D3 heav
41	239	68.1	445	18	T72337	Humanised reshaped
42	238.4	67.9	457	18	T72267	Mouse Mab 15 heavy
43	238.2	67.9	445	14	Q36530	Chimeric MAB heavy
44	238.2	67.9	445	14	Q36537	BR55-2 heavy chain
45	238.2	67.9	491	14	Q36535	BR55-2 murine IgG3

ALIGNMENTS

RESULT 1

ID V49820 standard; DNA; 351 BP.

XX V49820;

XX 02-NOV-1998 (first entry)

DE Vitaxin antibody heavy chain variable region DNA.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 1..351

FT /*tag= a

FT /product= "vitaxin antibody heavy chain variable region"

FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

```
XX WPI: 1998-437472/37.
DR P-PSDB; W76001.
XX
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
XX Claim 3; Fig 1a; 129pp; English.
XX
CC This sequence encodes the vitaxin antibody variable heavy chain region.
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match      100.08; Score 351; DB 19; Length 351;
Best Local Similarity 100.08; Pred. No. 5.9e-100; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0;

QY 1 CAGGTGCAGCTCTGGAGTCTGGGGAGGCGTGTGTGCAGCTTGGAGGTCCCTGAGACTC 60
DB 1 caggTgcagctgtgagtcgtggggaggcggtgtgagcgtggaggtccctgagactc 60
QY 61 TCCGTGTCAGCTCTGGAGTACCTTACCTTACCTAGTATGACATGCTTGGTTCGCCAGGCT 120
DB 61 tccgtgagcctctggattccctcagtagctatgacatgtctgggttgcgcaggct 120
QY 121 CCGGCGAGGGTCTGGAGTGGTGCAGAAAGTACGTAGTGGTGGTGGTACCTACTAT 180
DB 121 cccggcaggggtctggagtggtgcgaaagttagtgggtggtagcaccctactat 180
QY 181 TTAGACTGTGTCAGGCGGATTCACCATCTCCAGAGCAATAGTAAGAACACCCCTATAC 240
DB 181 ttagactgtgcaggcgagattcaccatctccagagacaatagtaagaacaccctatac 240
QY 241 CTGCAATGAACCTCTCTGAGAGCCGAGGACACAGCCGCTGATATTACTGTGCAAGACATAAC 300
DB 241 ctgcaaatgaactctctgagagccgaggacacagccgtgtattactgtgcaagacataac 300
QY 301 TACGCGAGTTTGGCTTACTGCGGCCAAGGACTACAGTGACGTGTTCTAGT 351
DB 301 tacgcgagtttggcttactgcgggccaaaggactacagtgactgtttctagt 351

RESULT 2
V49822
ID V49822 standard; DNA; 351 BP.
XX
AC V49822;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 antibody heavy chain variable region DNA fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
```

```
Key Location/Qualifiers
CDS 1..351
FT /tag= a
FT /product= "LM609 antibody heavy chain variable region"
FT /note= "partial sequence, no start or stop codon given"
W09833919-A2.
PD 06-AUG-1998.
XX
XX 30-JAN-1998; 98WO-US01826.
XX
XX 30-JAN-1997; 97US-0791391.
XX
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 3; Fig 2a; 129pp; English.
XX
XX This sequence encodes the LM609 antibody variable heavy chain region.
XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match      86.18; Score 302.2; DB 19; Length 351;
Best Local Similarity 91.98; Pred. No. 8.7e-85;
Matches 319; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGGTGCAGCTCTGGAGTCTGGGGAGGCGTGTGTGCAGCTTGGAGGTCCCTGAGACTCT 61
DB 2 aagTgcagctgtgagtcgtggggaggcgttagtgaagcctggaggtccctgagactct 61
QY 62 CCTGTGCAGCTCTGGAGTTCACCTTACCTAGTATGACATGCTTGGTTCGCCAGGCTC 121
DB 62 cctgtgcagcctctggattcgtcttcagtagctatgacatgtcttgggttcgcagattc 121
QY 122 CGGCAAGGGTCTCTGAGTGGGTTCGCAAAAGTATAGTGGTGGTAGCACCTACTATT 181
DB 122 cggagaagagcgtgagtggtgcgaaagttagtgggtggtagcaccctactatt 181
QY 182 TAGACACTGTGCGAGCGCGGATTCACCATCTCCAGAGCAATAGTAAGACACCCCTATACC 241
DB 182 tagacactgtgcagggcgcatccatctccagagacaatgccaagaacaccctatacc 241
QY 242 TGAATGAACCTCTCTGAGAGCCGAGGACACAGCCGCTGTTACTGTGCAAGACATAACT 301
DB 242 tgaatgaagcagctctgaactctgagacacagccatgtattactgtgcaagacataact 301
QY 302 ACGCAGTTTTCCTTACTGGGCGCAAGGACTACAGTACTGACTGTTTCT 348
DB 302 acgcagttttccttactgggccaagggaactctggctcactgtctct 348

RESULT 3
Q05555
```

ID Q05555 standard; DNA; 482 BP.

XX Q05555;

AC Q05555;

DT 10-DEC-1990 (first entry)

XX Sequence encoding variable region of murine AHT 54 heavy chain.

DE Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;

XX Mus sp.

OS

XX Key Location/Qualifiers

FT CDS 75..482

FT /*tag= a

XX EP380068-A.

XX 01-AUG-1990.

XX 24-JAN-1990; 90EP-0101351.

XX 04-DEC-1989; 89US-0441702.

XX 24-JAN-1989; 89US-0301216.

XX (MOLE-) MOLECULAR THERAPEU.

XX Zerler B;

XX WPI; 1990-232892/31.

XX P-PSDB; R06251.

XX Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region
XX
XX Disclosure; ; P; English.
XX
XX MABS comprising mouse CH and CL constant regions which human
CC variable regions may be used to create mouse/human hybrid MABS,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX
XX Sequence 482 BP; 112 A; 116 C; 130 G; 124 T; 0 other;

Query Match 76.5%; Score 268.6; DB 11; Length 482;

Best Local Similarity 85.9%; Pred. No. 2.7e-74; Indels 0; Gaps 0;

Matches 298; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 2 AGGTGACGCTGTGGAGTCTGGGGAGCGCTGTGTCAGCCTGGAGGTCCTCGAGACTCT 61

Db 133 aagtcagctgtgagctctggggagccttagtagaagcctggaggtccctgaaactct 192

Qy 62 CCTGTGACGCTCTGGATTCACCTTCAGTAGTATGACATGCTTTGGTTCGCCAGGCTC 121

Db 193 cctgtgagcctctggtattcgctttcagtagcattgacatgcttgggtggtccagactc 252

Qy 122 CGGGCAAGGCTCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTATT 181

Db 253 cggagaagagctgtgagtggtggtcgatacattagtagtgggtggtgatacacctactatc 312

Qy 182 TAGACATGTGACGGCGGATTCACCATCTCCAGACAAATAGTAAGAACACCCATATACC 241

Db 313 cagacactgtgaagggccgattccattccattccagagacaatgccaaagaccctttacc 372

Qy 242 TGCAATGAACCTCTGTAGAGCCGAGGACACAGCCGCTGTATTACTGTGCAAGACATACT 301

Db 373 tgcgaatagcagctctgaagctgtgagcacagccgctgtattactgtgcaagaggtacg 432

Qy 302 ACGGCAAGTTTGTCTACTTGGGGCCCAAGGACTACAGTACTGTTTCT 348

Db 433 gctccctttgttacttggggcccaaggactctggtcactgtctct 479

RESULT 4

Q62804

XX Q62804 standard; DNA; 417 BP.

AC Q62804;

DT 25-JAN-1995 (first entry)

XX Humanised murine KC-4 immunoglobulin heavy chain V-region DNA.

XX Immunoglobulin variable domain; primer; polymerase chain reaction;
KW Chimeric antibody; human mammary fat globule; human breast carcinoma;
KW murine anti-HMFG monoclonal antibody KC-4; humanised analogue; ss.
XX Chimeric Mus musculus.
OS Chimeric Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..416

FT /*tag= a

FT /note= "humanised KC-4 VH chain"

FT mat_peptide 58..416

FT /*tag= b

FT /product= heavy_chain_V-region

FT /note= "humanised framework region"

XX WO9411509-A.

XX 26-MAY-1994.

XX 16-NOV-1993; 93WO-US11445.

XX 16-NOV-1992; 92US-0977696.

XX 30-SEP-1993; 93US-0129930.

XX 08-OCT-1993; 93US-0134346.

XX (CANC-) CANCER RES FUND CONTRA COSTA.

XX Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;

XX WPI; 1994-183510/22.

XX P-PSDB; R52823.

XX New analogue peptide(s) comprising antibody variable regions -
PT used to develop prods. for use in the detection, diagnosis,
PT therapy and prevention of neoplasms
XX
XX Example 67; Page 91; 109pp: English.
XX
XX This DNA sequence encodes a humanised murine anti-human carcinoma
CC antibody heavy chain variable region. The humanised antibody is
CC useful for carcinoma therapy and diagnosis and for in vivo imaging
CC of neoplastic cells. It is also of use in inhibiting the growth of
CC a primary or metastasised neoplasm.
XX
XX Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;

Query Match 75.2%; Score 263.8; DB 15; Length 417;

Best Local Similarity 85.8%; Pred. No. 8e-73;

Matches 308; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

Qy 2 AGGTGACGCTGTGGAGTCTGGGGAGCGCTGTGTCAGCCTGGAGGTCCTCGAGACTCT 61

Db 59 aagtcagactgtgagctctggggagccttagtagcagcctggaggtccctgagactct 118

Qy 62 CCGTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCTTTGGTTCGCCAGGCTC 121

Db 119 cctgtgcagcctctggattccttccagtagctatgccatgctcttgggttcgaggtc 178

Qy 122 CGGGCAAGGCTCTGAGTGGGTGCGCAAAAGTTAGTAGTGGTGGTAGCACCTACTATT 181

Db 179 cagggaagggtgagtggtgcagaaattagtagtggtgtaattacgactactatc 238
QY 182 TAGACACTGTGAGGCCGATTCACCATCTCCAGACACATAGTAGACACACCTATACC 241
Db 239 aagacactgtgagcgccgactccacatctccagagacaaattcccaagaacacccctgtacc 298
QY 242 TGCAAATGAACCTCTGTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 299 tgcaaatgaactgtgagcgctgagacacgcccgtgtattactgtgcaaggaggact 358
QY 302 ACGG-----CAGTTTGTCTACTGGGCCAGGGGACTACAGTGAAGTCTTCTAGT 351
Db 359 acggtatcccgccgtgtgttactggtggccaaaggagactctgtcactgtctctagt 417

RESULT 5
Q87534
ID Q87534 standard; DNA; 417 BP.
XX
AC Q87534;
XX
DT 27-OCT-1995 (first entry)
XX
DE Humanised anti-KC-4 antibody VH FR-H2.
XX
KW Anti-KC-4 antibody; humanised antibody; cancer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..417
FT /*tag= a
XX
XX WO9510776-A.
XX
PD 20-APR-1995.
XX
XX 16-NOV-1993; 93WO-US11444.
XX
XX 08-OCT-1993; 93US-0134346.
XX
PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
XX
PI Ceriani RL, Docouto JJR, Peterson JA;
XX
XX WPI: 1995-161912/21.
DR P-PSDB; R70471.
XX
XX New humanised anti-KC-4 monoclonal antibody - used for detection of
PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
PT cancers
XX
XX Claim 23; Table 22, Page 46; 61pp; English.
XX
XX Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma APCC
CC HB 8710 (US4708930). The murine variable regions were modified at
CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
CC humanised DNA sequences for the VH and VL segments are shown in
CC Q87534 and Q87533 respectively. Plasmid constructions comprising
CC the humanised variable regions and the human constant regions were
CC then used to transform SP2/0-Ag14 myeloma cells to produce the
CC humanised anti-KC-4 MAbs. The deduced AA sequences of the
CC humanised anti-KC-4 variable light and heavy chains are given in
CC R70470 and R70471 respectively.
XX
XX Sequence 417 BP; 85 A; 95 C; 128 G; 109 T; 0 other;
SQ

Query Match 75.2%; Score 263.8; DB 16; Length 417;
Best Local Similarity 85.8%; Pred No. 86-73;
Matches 308; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
QY .2 AGTGCAGCTGTGGAGTCTGGGGAGGCGTTGTGCGCCTGGAAGGTCCTCGAGACTCT 61

Db 59 aagtgacagatggtgagctgtggggagggttagtgacgcctggagggtccctgagactct 118
QY 62 CCTGTGACGCTCTGGATTACCTTCAGTAGCTATGACATGCTTGGTTCCGCCAGGCTC 121
Db 119 cctgtgcagctctggattccttctcagtagctagccttcttgggttcgcagggctc 178
QY 122 CGGCAAGGGTCTGGAGTGGGTGCGAAAGTTAGTGTGGTGGTAGCACCCTACTATT 181
Db 179 cagggaagggtgagtggtgcagaaattagtagtggtgtaattacgactactatc 238
QY 182 TAGACACTGTGAGGCCGATTCACCATCTCCAGACACATAGTAGACACACCTATACC 241
Db 239 aagacactgtgagcgccgactccacatctccagagacaaattcccaagaacacccctgtacc 298
QY 242 TGCAAATGAACCTCTGTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
Db 299 tgcaaatgaactgtgagcgctgagacacgcccgtgtattactgtgcaaggaggact 358
QY 302 ACGG-----CAGTTTGTCTACTGGGCCAGGGGACTACAGTGAAGTCTTCTAGT 351
Db 359 acggtatcccgccgtgtgttactggtggccaaaggagactctgtcactgtctctagt 417

RESULT 6
T90020
ID T90020 standard; DNA; 582 BP.
XX
AC T90020;
XX
DT 12-DEC-1997 (first entry)
XX
DE DNA encoding heavy chain variable region of human CRA2 antibody.
XX
KW Complementarity determining region; CDR: murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IGE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2; ds.
XX
OS Homo sapiens.
XX
XX JP09191886-A.
XX
XX 29-JUL-1997.
XX
XX 19-JAN-1996; 36JP-0024816.
XX
XX 19-JAN-1996; 96JP-0024816.
XX
XX (ASAK) ASAHI BREWERIES LTD.
XX (NIKK-) NIKKA WHISKEY KK.
XX (TORI) TORII YAKUHIN KK.
XX (TSUR/) TSURA T.
XX
XX WPI: 1997-429186/40.
XX
XX Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IGE receptor - useful medicinally and have low
PT antigenicity in humans
XX
XX Disclosure: Fig 9; 26pp; Japanese.
XX
XX The present sequence, which encodes the heavy chain variable
CC region of the human antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAb), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAb. The humanised,
CC semi-chimeric or chimeric MAb can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
XX
XX Sequence 582 BP; 133 A; 134 C; 155 G; 160 T; 0 other;
SQ

CC	produced using the method of the invention. The method is for preparing
CC	an antibody Fab-fragment using the yeast Pichia pastoris as the host
CC	cell. The method can prepare an antibody Fab fragment cost efficiently
CC	and in high yield.
XX	
SQ	Sequence 761 BP; 166 A; 228 C; 206 G; 161 T; 0 other;
Query Match 74.0%; Score 259.6; DB 20; Length 761;	
Best Local Similarity 84.4%; Pred. NO. 2e-71;	
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps	
QY	2 AGGTGCAGCTGTTGGAGTCTGGGGGAGGCCCTTGTCAGCCTCGAAGGTCCCTGAGACTCT 61
DB	
DB	92 aggtgcagctggtggagtctggggaggcttggtccagcctgggggtccctgagactct 151
QY	62 CCNGTGCAGCCTCTGGATTACACCTTCAGTAGCTATGACATGTCCTTGGTTTCGCCAGGCTC 121
DB	
DB	152 ccngtgcagcctctggattcaccttttagtaccatccccatgcttcctgggtccgccaggctc 211
QY	122 CGGGCAAGGGTCTGGAAGTGGGTGCGCAAAAGTATTAGTAGTGGTGGTGTAGCACCTACTATT 181
DB	
DB	212 cagggaaagggtcgagtggtggctccaftagtaatgctggtgtagcacctactatc 271
QY	182 TAGACACTGTGCAGGCCGATTCACCATCTCCAGAGACAATAGTAGAACACCCCTATACC 241
DB	
DB	272 cagacactgtaaaagggccgattcaccatctccagagacaacgaagaactcaactgtatc 331
QY	242 TGCAAAATGAACCTCTCTGAGAGCGGAGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB	
DB	332 tgc aaatgaacagcccagagccgagacacggctgtgtattactgtcgagacataatt 391
QY	302 ACGGCAGTTTTGCTTACTGGGGCCAAGGGACTACAGTACTGTTTC 347
DB	
DB	392 atggagaatggactactgggggcaaggacacgggtcacccgtc 437
RESULT	8
XO1216	
ID	XO1216 standard; cDNA to mRNA; 770 BP.
XX	
AC	XO1216;
DT	
XX	
DE	31-MAR-1999 (first entry)
XX	
KW	Human antiFc epsilon RI alpha chain antibody coding sequence #4.
XX	
OS	AntiFc epsilon RI alpha chain antibody; antibody production; human; ds.
XX	
XX	Homo sapiens.
Key	Location/Qualifiers
CDS	: 34..762
FT	/*tag= a
FT	:
FT	sig_peptide : 34..99
FT	/*tag= b
FT	:
FT	mat_peptide : 100..759
FT	/*tag= c
XX	
PX	JP11000174-A.
XX	
PD	06-JAN-1999.
XX	
PF	13-JUN-1997; 97JP-0171232.
XX	
PR	13-JUN-1997; 97JP-0171232.
XX	
PA	(ASAK) ASahi BREWERIES LTD.
PA	(NIKK-) NIKKA WHISKEY KK.
PA	(TORI) TORII YAKUHIH KK.
PA	(TSUR/) TSURA T.
XX	
DR	WPI; 1999-124394/11.

```
DR P-PSDB; W73876.
XX
PT Preparing an antibody Fab fragment using yeast - in high yield
XX
XX Claim 6; Page 9-10; 13pp; Japanese.
XX
CC This sequence encodes a human antiFc epsilon RI alpha chain antibody,
CC produced using the method of the invention. The method is for preparing
CC an antibody Fab fragment using the yeast Pichia pastoris as the host
CC cell. The method can prepare an antibody Fab fragment cost efficiently
CC and in high yield.
XX
SQ Sequence 770 BP; 172 A; 223 C; 205 G; 170 T; 0 other;

Query Match 74.0%; Score 259.6; DB 20; Length 770;
Best Local Similarity 84.4%; Pred. No. 2e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGCGAGCTGGAAGGTCCCTGAGACTCT 61
DB 101 aggtgcagctgtggaagtcctgggagagcttggtccagcctgggggtccctgagactct 160
QY 62 CCGTGCAGCCTCTGATTCATCTCAGTAGCTATGACATGCTCTGGGTTCGCCAGGCTC 121
DB 161 cctgtgcagcctctggtacccttttagtaccctccatctctgtggtccgaggtc 220
QY 122 CGGCAAGGCTGTGGAGTGGTGCNAAAGTTAGTAGTGTGTGTAGTGTGTGTGTGT 181
DB 221 cagggaagggtgtgagtggtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 280
QY 182 TAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAAATAGTAAGAACACCCATACC 241
DB 281 cagacactgaaggccgattccaccatctccagagacacccaaagaaactcactgtatc 340
QY 242 TGAATGAACTCTGTGAGCGGAGGACACAGCCGCTGTATTACTGTGCAAGACATAACT 301
DB 341 tgcataatgaacgcctgagagcgcgagacacgcgtgtgtattactgtgcagacataatt 400
QY 302 ACGGCGATTTTCTTACTGCGGCCAGGAGGACTACAGTGTGCTTTC 347
DB 401 atggagggaatgactactctggggcaaggagaccacggtccaccgtctc 446

RESULT 9
Q58650
ID Q68650 standard; DNA; 413 BP.
XX
AC Q68650;
XX
DT 13-FEB-1995 (first entry)
XX
DE MAB A33 heavy chain coding sequence.
XX
KW Polymerase chain reaction; primer; amplify; PCR; variable region; light;
KW heavy; chains; VL; VH; humanised; antibody; vectors; expression; human;
KW secretion; A33; Fab'(gamma/delta/cys); pC16; ompA signal; C-kappa;
KW pSKompa; pMR055; CH1 domains; hinge; deltaCys; pMR022; pR0109;
KW antigen; diagnosis; treatment; colorectal cancer; metastases; ss.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT primer_bind 1..32 /*tag= a
FT CDS 6..413 /*tag= b
FT sig_peptide 6..62 /*tag= c
FT mat_peptide 63..413 /*tag= d
FT primer_bind 396..413
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FT XX /*tag= e
PN WO9413805-A.
XX
PD 23-JUN-1994.
XX
PF 10-DEC-1993; 93WO-GB02529.
XX
PR 10-DEC-1992; 92GB-0025853.
PR 22-JUL-1993; 93GB-0015249.
XX
PA (CLLT ) CELLTech LTD.
XX
XX Adair JR, King DJ, Owens RJ;
XX
DR WPI: 1994-217881/26.
DR P-PSDB; R56962..
XX
PT Humanised antibodies raised against A33 antigen - are used for
PT diagnosis or treatment of colorectal tumours and metastases
XX
PS Example 1; Fig 3(ii); 90pp; English.
XX
CC The sequences given in Q68649-50 encode the light and heavy chain
CC variable regions (VH and VL) of the humanised anti-A33 antibody of
CC the invention. These fragments were produced by PCR using the primer
CC sequences given in Q68624-48. The amplified fragments were used in the
CC construction of vectors for the expression and secretion of the chimeric
CC humanised A33. The amplified products were cleaved with BstBI and SphI
CC for the light chain and HindIII and ApaI for the heavy chain. These
CC fragments were cloned into the human kappa light chain acceptor vector,
CC pMR15.1, and the human heavy chain, IgG1, acceptor vector, pMR011
CC respectively, to give chimeric expression vector pR0108 for the light
CC chain and pR0107 for the heavy chain. Proteins which bind the A33
CC antigen can be used in the diagnosis or treatment of colorectal cancers
CC and metastases.
XX
SQ Sequence 413 BP; 88 A; 98 C; 117 G; 108 T; 2 other;

Query Match 73.3%; Score 257.4; DB 15; Length 413;
Best Local Similarity 83.9%; Pred. No. 7.8e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGCGAGCTGGAAGGTCCCTGAGACTCT 61
DB 64 aagtgaagctgtgtgagtcctggggagagccttagtgaagcctggaggggtccctgaaactct 123
QY 62 CCGTGCAGCCTCTGATTCATCTCAGTAGCTATGACATGCTCTGGGTTCGCCAGGCTC 121
DB 124 cctgtgcagcctctggtacccttttagtaccctatgacatgctgtgtgtgtgtgtgtgtgt 183
QY 122 CGGCAAGGCTGTGGAGTGGTTCGCCAAAGTTAGTAGTGTGTGTGTGTGTGTGTGTGT 181
DB 184 cggagaagagctgtgagtggtgtgcacaccattagtagtgggtgtgtgtgtgtgtgtgtgtgt 243
QY 182 TAGACACTGTGAGGCGCCGATTCACCATCTCCAGAGACAAATAGTAAGAACACCCATACC 241
DB 244 tagacagtgtgaaggccgattccaccatctccagagacagtgccaggaacacctatacc 303
QY 242 TGAATGAACTCTCTGAGAGCCGAGGACACAGCGGTGTATTACTGTGCAAGACATAACT 301
DB 304 tgcataatgaacgcctgagagcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 363
QY 302 ACGGCGATTTTCTTACTGCGGCCAGGAGGACTACAGTGTGCTTTC 348
DB 364 tagtcccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 410

RESULT 10
V99765
ID V99765 standard; DNA; 721 BP.
XX
```


AC	V9765;
XX	23-MAR-1999 (first entry)
DT	A33/212 single-chain Fv coding sequence.
XX	Linker; fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
KW	multichain protein; immunoglobulin; single chain antibody Fv; cancer;
KW	aggregation; ds.
XX	Synthetic.
OS	
XX	Key Location/Qualifiers
FH	CDS 1..711
FT	/tag= a
FT	/product= "A33/212 scFv"
FT	/note= "the start codon is not indicated"
FT	misc_feature 1..321
FT	/tag= b
FT	/note= "sequence coding for A33 VL region"
FT	misc_feature 322..363
FT	/tag= c
FT	/note= "sequence coding for peptide linker 212"
FT	misc_feature 364..708
FT	/tag= d
FT	/note= "sequence coding for A33 Vh region"
XX	US5856456-A.
PN	05-JAN-1999.
PD	07-APR-1994; 94US-0224591.
PF	07-APR-1994; 94US-0224591.
XX	20-NOV-1992; 92US-0980529.
PR	15-JAN-1993; 93US-0002845.
XX	(ENZO-) ENZON INC.
PA	Filpula DR, Whitlow MD;
PI	WPI; 1999-105193/09.
DR	P-PSDB; W95440.
XX	DNA encoding fusion polypeptide including protease resistant linker
PT	- for making single-chain Fv antibody fragments, e.g for diagnosis
PT	and treatment of cancer
XX	Disclosure; Fig 12; 39pp; English.
PS	The invention is directed to a novel peptide linker useful for connecting
XX	polypeptide constituents into a novel linked fusion polypeptide. The
CC	peptide linker includes at least one XP motif (where X is a charged
CC	amino acid) and includes any of these sequences (GSTSGCGPSSGEGSTKG;
CC	GTSXGSPSGESTKG; or GSTSGKSEKG) to inhibit its proteolysis by
CC	subtilisin or trypsin. DNA molecules encoding fusion polypeptides
CC	containing two polypeptides, derived from the same multichain protein of
CC	the immunoglobulin (Ig) superfamily and a peptide linker as above, are
CC	particularly used to prepare single chain antibody Fv fragments (scFv),
CC	potentially useful for diagnosis and treatment of cancer. The fusion
CC	polypeptide containing the specified linkers is proteolytically stable
CC	(associated with positioning of the P residue) and resistant to
CC	aggregation, while residue X improves solubility. The present sequence
CC	represents the nucleotide sequence of a A33/212 scFv fragment.
XX	Sequence 721 BP; 176 A; 172 C; 189 G; 184 T; 0 other;
SQ	
Query Match	73.3%; Score 257.4; DB 20; Length 721;
Best Local Similarity	83.9%; Pred. No. 9.6e-71;
Matches 291; Conservative	0; Mismatches 56; Indels 0; Gaps 0;
QY	2 AGGTGCAGCTGGTGGAGTCGTGGGGAGCGTTGTGCAGCCTGGGAAGTGCTCCCTGAGACTCT 61

Best Local Similarity 83.9%; Pred. No. 9.6e-71; Mismatches 0; Conservative 0; Gaps 0;

QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTCAGAGCTGGAAGGTCCTGAGACTCT 61
DB 365 aagtgaagctgtggagctggggaggttagtgagcctggaggtccctgaaactct 424

QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTGGCAGGCTC 121
DB 425 cctgtgagcctctggattcgtttcagttacattgacatgtcttgggttgcagactc 484

QY 122 CGGGCAAGGCTCTGAGTGGGTGGCAAAAGTTAGTAGTGTGTGTGAGCAGCTACTATT 181
DB 485 cggagaagagctggagtggtgcaaccatttagttagtggttagttacactactatt 544

QY 182 TAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACAATAGTAGAACACCCCTATAC 241
DB 545 tagacagtgtgaagggccattccaccattccagagacagtgccaggaaacccctatac 604

QY 242 TGCAAATGAACCTCTGAGAGCGGAGGACACAGCCCTGTATTACTGTGCAAGACATAACT 301
DB 605 tgcaaatgacagctcagagctgagagacacggcctgtattactgtgacagactacgg 664

QY 302 AGGCGAGTTTGTCTACTGGGCGCAAGGAGCTACAGTACTGTTTCT 348
DB 665 tagtcccgcttgcctactgggccaaggagactctgtgctactgtctct 711

RESULT 12
V99766
ID V99766 standard; DNA; 733 BP.
XX AC V99766;
XX DT 23-MAR-1999 (first entry)
XX DE A33/218 single-chain Fv coding sequence.
KW Linker: fusion polypeptide; proteolysis; subtilisin; trypsin; scFv;
KW multichain protein; immunoglobulin; single chain antibody Fv; cancer;
KW aggregation; ds.
XX OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..711
FT /tag- a
FT /product- "A33/218 scFv"
FT /note- "the start codon is not indicated"
FT misc_feature 1..321
FT /tag- b
FT /note- "sequence coding for A33 V1 region"
FT misc_feature 322..375
FT /tag- c
FT /note- "sequence coding for peptide linker 218"
FT misc_feature 376..708
FT /tag- d
FT /note- "sequence coding for A33 Vh region"
XX US5856456-A.
XX PD 05-JAN-1999.
XX PF 07-APR-1994; 94US-0224591.
XX PR 07-APR-1994; 94US-0224591.
XX PR 20-NOV-1992; 92US-0980529.
XX PR 15-JAN-1993; 93US-0002845.
XX PA (ENZO-) ENZON INC.
XX PI Filpula DR, Whitlow MD;
XX XX

DR WPI; 1999-105193/09.
DR P-PSDB; W95441.
XX DNA encoding fusion polypeptide including protease resistant linker
PT - for making single-chain Fv antibody fragments, e.g for diagnosis
PT and treatment of cancer
XX
PS Disclosure; Fig.13; 39pp; English.
XX
CC The invention is directed to a novel peptide linker useful for connecting
CC polypeptide constituents into a novel linked fusion polypeptide. The
CC peptide linker includes at least one XP motif (where X is a charged
CC amino acid) and includes any of these sequences (GTSXGSGXGSGSGXGK;
CC GTSXGSPSGSGXGK; or GTSXGSEKKG) to inhibit its proteolysis by
CC subtilisin or trypsin. DNA molecules encoding fusion polypeptides
CC containing two polypeptides, derived from the same multichain protein of
CC the immunoglobulin (Ig) superfamily and a peptide linker as above, are
CC particularly useful to prepare single chain antibody Fv fragments (scFv),
CC potentially useful for diagnosis and treatment of cancer. The fusion
CC polypeptide containing the specified linkers is proteolytically stable
CC (associated with positioning of the P residue) and resistant to
CC aggregation, while residue X improves solubility. The present sequence
CC represents the nucleotide sequence of a A33/218 scFv fragment.
XX
SQ Sequence 733 BP; 179 A; 175 C; 196 G; 183 T; 0 other;

Query Match 73.3%; Score 257.4; DB 20; Length 733;
Best Local Similarity 83.9%; Pred. No. 9.6e-71;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTCAGAGCTGGAAGGTCCTGAGACTCT 61
DB 377 aagtgaagctgtggagctggggaggttagtgagcctggaggtccctgaaactct 436

QY 62 CCGTGTGACGCTCTGATTCACCTTCAGTAGCTATGACATGCTTGGGTTGGCAGGCTC 121
DB 437 cctgtgagcctctggattcgtttcagttacattgacatgtcttgggttgcagactc 496

QY 122 CGGGCAAGGCTCTGAGTGGGTGGCAAAAGTTAGTAGTGTGTGAGCAGCTACTATT 181
DB 497 cggagaagagctggtgag-999tcgcaaccattagtagtgggttgcagactactatt 556

QY 182 TAGACACTGTGAGGCGCGATTCACCATCTCCAGAGACAATAGTAGAACACCCCTATAC 241
DB 557 tagacagtgtgaagggccattccaccattccagagacagtgccaggaaacccctatac 616

QY 242 TGCAAATGAACCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGACATAACT 301
DB 617 tgcaaatgacagctcagagctgagagcagcgctgtattactgtgacagactacgg 676

QY 302 AGGCGAGTTTGTCTACTGGGCGCAAGGAGCTACAGTACTGTTTCT 348
DB 677 tagtcccgcttgcctactgggccaaggagactctgtgctactgtctct 723

RESULT 13
237398
ID 237398 standard; DNA; 733 BP.
XX AC 237398;
XX DT 08-FEB-2000 (first entry)
XX DE Linked fusion protein A33/218 scFv coding sequence.
XX Fusion protein; linker; linked fusion polypeptide; multichain protein;
KW protein complex; antibody; ss.
XX Synthetic.
XX PN US5990275-A.
XX XX

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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 05:03:45 ; Search time 75.17 Seconds
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Title: US-08-790-540A-1
Perfect score: 351
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 561672
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.4	73.3	413	1	US-08-253-877C-56
2	257.4	73.3	413	2	US-08-452-164A-56
3	257.4	73.3	721	2	US-08-224-591-15
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5	257.4	73.3	733	2	US-08-224-591-17
6	257.4	73.3	733	2	US-08-926-789-17
7	246.8	70.3	1329	4	PCT-US96-13152-3
8	244.8	69.7	418	1	US-07-977-696C-27
9	244.8	69.7	418	1	US-08-129-930B-27
10	240.6	68.5	360	2	US-08-672-176A-3
11	240.6	68.5	720	2	US-08-672-176A-5
12	239.8	68.3	357	1	US-08-475-000-15
13	239.8	68.3	357	2	US-08-483-199-15
14	239.8	68.3	357	2	US-08-484-508-15
15	238.2	67.9	445	1	US-08-053-171-10
16	238.2	67.9	491	1	US-08-053-171-6
17	237.2	67.6	717	2	US-08-553-497A-17
18	236.6	67.4	717	2	US-07-956-399-3
19	235.6	67.1	357	1	US-08-331-398A-21
20	235.6	67.1	357	1	US-08-207-996-26
21	235.6	67.1	357	2	US-08-760-840A-26
22	235.6	67.1	357	2	US-08-760-840A-27
23	235.6	67.1	357	2	US-08-331-397B-21
24	235.6	67.1	357	2	US-08-759-804A-21
25	235.6	67.1	357	3	US-09-266-119-26
26	235.6	67.1	357	3	US-09-266-119-27
27	235.6	67.1	375	1	US-08-331-398A-59
28	235.6	67.1	375	2	US-08-331-397B-59

29	235.6	67.1	375	2	US-08-759-804A-58
30	235.6	67.1	738	1	US-08-331-398A-31
31	235.6	67.1	738	2	US-08-331-397B-31
32	235.6	67.1	738	2	US-08-759-804A-31
33	235.4	67.1	923	4	PCT-US94-07659-1
34	234.8	66.9	417	1	US-08-398-613A-21
35	234.8	66.9	417	1	US-08-398-612A-21
36	234.8	66.9	417	1	US-08-398-611A-21
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38	234.8	66.9	417	2	US-08-491-334A-21
39	234.8	66.9	417	3	US-09-027-449-18
40	234.8	66.9	417	3	US-08-804-444A-18
41	234.8	66.9	417	3	US-09-026-985-18
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45	234.8	66.9	756	1	US-08-396-851A-29

ALIGNMENTS

RESULT 1
US-08-253-877C-56
; Sequence 56, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tscu, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne New Jersey
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253.877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: "nucleic acid"
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; MOLECULE TYPE: CDNA
; NAME/KEY: CDS
; LOCATION: 6..413
US-08-253-877C-56

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Query Match          73.38; Score 257.4; DB 1; Length 413;
Best Local Similarity 83.9%; Pred. No. 3.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      2 AGGTGCAGCTGGTGGAGTGCTGGGAGGCGGTGTGTCAGCCTGGAAAGTCCCTGGAGACTCT 61
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY     64 AAGTGAAGCTGGTGGAGTCTGGGGAGGCTTAGTGAACCTGGAGGGTCCCTGAACACTCT 123
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY     62 CCTGTGCAGCCTCTGGATTCACCTTTCACTAGTACGTATGACATGCTCTGTGGTTCGCCAGGCTC 121
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    124 CCTGTGCAGCCTCTGGATTCGCTTTCACTACCTATGACATGCTCTGTGGTTCGCCAGACTC 183
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    122 CGGCAAGGCTCTGGAGTGGCTGCCAAGTACTAGTGGTGGTGGTAGCACCTACTATT 181
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    184 CGGAGAAGAGCTGGAGTGGGTGCGAACCATAGTAGTGGTGGTAGTTACACCTACTATT 243
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    182 TAGACACTGTGCAGGGCGCGATTTCACCATTCTCCAGAGACAATAGTAAGAACACCCCTATAACC 241
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    244 TAGACAGTGTGAAGGCGGATTTCACCATCTCCAGAGACAGTCCCAGGAACACCCCTATAACC 303
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    242 TCCAATGAACCTCTCTGAGAGCCGAGGACACAGCGGTGTATCTGTGTCAGACACATAACT 301
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    304 TGCAAATGAGCAGCTCTGAGGTCTGAGGACACGGGCTTGTATCTACTGTGCACCGACTACGG 363
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    302 ACGCCAGTTTTGCTTACTTGGGCGCAAGGGACTACAGTCACTGTTTCT 348
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    364 TAGTCCCGTTGCTTACTTGGGCGCAAGGGACTCTGGTCACCGTCTCT 410
DB      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
US-08-452-164A-56
; Sequence 56, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```


CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723)
US-08-224-591-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;
Best Local Similarity 83.9%; Pred. No. 4.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 121
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 436
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 121
DB 437 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 496
QY 122 CGGCAAGAGGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 181
DB 497 CGGCAAGAGGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 556
QY 182 TAGACACTGTGACAGGCGCGATTCCACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241
DB 557 TAGACAGTGTGAAGGCGCGATTCCACCATCTCCAGAGAGAGTCCAGAGAACCCCTATACC 616
QY 242 TCGAATGAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 301
DB 617 TCGAATGAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 676
QY 302 ACGGCAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 348
DB 677 TAGTCCCGTTGCTTACTGGGCGCAAGGAGGACTCTGGTCACTGCTCT 723

RESULT 6
US-08-926-789-17
Sequence 17, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,591
FILING DATE:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723)
US-08-926-789-17

Query Match 73.3%; Score 257.4; DB 2; Length 733;
Best Local Similarity 83.9%; Pred. No. 4.2e-77;
Matches 291; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 2 AGGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 61
DB 377 AAGTGAAGCTTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 436
QY 62 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 121
DB 437 CCTGTGACAGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 496
QY 122 CGGCAAGAGGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 181
DB 497 CGGCAAGAGGCTGTGGAGTCTGGGGAGGCGTTGTGACAGTATGACATGCTTGGGTTGCCAGGCTC 556
QY 182 TAGACACTGTGACAGGCGCGATTCCACCATCTCCAGAGACAATAGTAAGAACCCCTATACC 241
DB 557 TAGACAGTGTGAAGGCGCGATTCCACCATCTCCAGAGAGAGTCCAGAGAACCCCTATACC 616
QY 242 TCGAATGAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 301
DB 617 TCGAATGAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 676
QY 302 ACGGCAAGTCTGTGAGAGCGGAGGACAGACCGCTGTATTACTGTGCAAGACATTAAT 348
DB 677 TAGTCCCGTTGCTTACTGGGCGCAAGGAGGACTCTGGTCACTGCTCT 723

RESULT 7
PCT-US96-13152-3
Sequence 3, Application PC/TUS9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Norman D. Hanson
STREET: 805 Third Avenue

```

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1,1329
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1
PCT-US96-13152-3

Query Match 70.3%; Score 246.8; DB 4; Length 1329;
Best Local Similarity 84.1%; Pred. No. 2e-73;
Matches 291; Conservative 0; Mismatches 52; Indels 3; Gaps

QY 2 AGTGCAGCTGGTGGAGTCTGGGGGAGGCGTTGTGCAGCCTGGAGGTCCTCCCTGAGACTCT 61
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 AAGTCAACTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCTGGAGGAAGCTTTGAGACTCT 61
QY 62 CTGTGTCAACCTCTGGATTCACTTCAGTAGCTATGCATGTCTTGGGTGCCAGGCTC 121
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 CTGTGTCAACCTCTGGATTCACTTCAGTAGCTATGCATGTCTTGGGTGCCAGGCTC 121
QY 122 CGGGCAAGGCTCTGGAGTGGGTCCGAAAAGTTAGTAGTGGTGGTAGCACCTACTACTATT 181
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
122 CAGGGAAGGACTCGAGTGGTTCGATCATTAGTA--CTGGTGGTAGCACCTACTATC 178
QY 182 TAGACACTCTGAGGGCCGATTACCATCTCCAGAGACAATAAGTAGAACAACCCCTATACC 241
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
179 CAGACAGTGTGAAGGGCCGATTCCACCATCTCCAGAGATAATGCCAAGAACACCCCTGTACC 238
QY 242 TCCAAATGAACCTCTGTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCCAGACATAACT 301
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
239 TCCAAATGAATCTCTGAGGGCTGAGGACACAGCCGTGTATTACTGTGCCAGAGACTATG 298
QY 302 ACGGCAAGTTTGTCTACTGGGCCAAGGACTACAGTGTACTGTTC 347
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
299 ACGGCTATTTTACTACTGCGGCCAAGGACCCCTGGTCACTCTC 344

RESULT 8

```


RESULT 9

US-08-129-930B-27
; Sequence 27, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-129-930B-27

Query Match 69.7%; Score 244.8; DB 1; Length 418;
Best Local Similarity 82.9%; Pred No. 5,5e-73;
Matches 295; Conservative 0; Mismatches 52; Indels 9; Gaps 1;
QY 2 AGGTGCAGCTGGTGGAGTCTGGGGGAGCGTTGTGCAGCCTGGAAAGGTCCTCGAGACTCT 61
Db 59 AAGTCAGATGCTGGAGTCTGGGGAGGCTTAGTGAAGCCTGGAGGTCCTCGAAACTCT 118
QY 62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTAGCTAGTGTGATGCTTGGGTTCGCCAGGCTC 121
Db 119 CCTGTGCAGCCTCTGGATTCAGTTCGCTATGATGCTATGCTTGGGTTCGCCAGTCTC 178
QY 122 CGGGCAAGGGTCTGGAGTGGGTGCGAAAGTTAGTAGTGTGGTGGTAGCCTACTATT 181
Db 179 CAGAGAGAGGGCTGAGTGGGTGCGAGAAATTAGTAGTGGTGGTAACTAGCGCTACTATC 238
QY 182 TAGACACTGTGCGAGCGCCGATTCACCTATCTCCAGACATAAGTAAAGAACACCCCTATACC 241
Db 239 AAGACACTGTGACGGCGCGGATTCACCTATCTCCAGACATAAGTAAAGAACACCCCTGTACC 298
QY 242 TCGAATGACTCTCTGAGAGCGGAGGACACAGCCGTTACTTACTGTGCAAGACATAACT 301
Db 299 TGGAAATGAGCAGTCTGAGGTCTGAGGACACAGCCCATGTATTACTGTGCAAGGGAGGACT 358

QY 302 ACGG-----CAGTTTCTTACTGGGCCCAAGGAGCTACAGTACTGTTTCT 348
Db 359 ACGGTATCCCGCGCTGGTTGCTTACTGGGCCCAAGGAGCTCTGTTCTCTCTCT 414
RESULT 10
US-08-672-176A-3
; Sequence 3, Application US/08672176A
; Patent No. 5908925
; GENERAL INFORMATION:
; APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
; TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
; TITLE OF INVENTION: Specificity for Glycated Albumin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Exocell, Inc.
; STREET: 3508 Market Street, suite 420
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS 4.0 or better
; SOFTWARE: Wordperfect, Version 5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,176A
; FILING DATE: unknown
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Silver, Robert S.
; REGISTRATION NUMBER: unknown
; REFERENCE/DOCKET NUMBER: E1042/20002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2010
; TELEFAX: 215-751-1142
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs/120 amino acid residues
; TYPE: nucleic acid/amino acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: humanized A717 heavy chain variable region
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE: synthetic
; ORGANISM: N/A
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELL: N/A
; IMMEDIATE SOURCE: plasmid
; LIBRARY: N/A
; CLONE: PHU4717VH-1
; POSITION IN GENOME: N/A
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE: human framework regions; murine CDRs
; NAME/KEY: FR-1; CDR-1; FR-2; CDR-2; FR-3; CDR-3; FR-4
; LOCATION: aa#1-30; aa#31-35; aa#36-49; aa#50-66;
; LOCATION: aa#67-98; aa#99-109; aa#110-120

IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycosylated albumin
PUBLICATION INFORMATION: N/A

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 3:

US-08-672-176A-3

Query Match 68.5%; Score 240.6; DB 2; Length 360;

Best Local Similarity 82.3%; Pred. No. 1.3e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGTTGGGTTCGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGTTGGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
DB 122 CCGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
QY 182 TAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATAGTAGAAGACCCCTATACC 241
DB 182 TAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATAGTAGAAGACCCCTATACC 241
QY 242 TCGAATGAACCTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGA----- 294
DB 242 TCGAATGAACCTCTCTGAGAGCGGAGGACACAGCCGTGTATTACTGTGCAAGAGATGTT 301
QY 295 --CATAACTACGGCAGTTTGTCTTACTGGGGCCAGGGGACTACAGTACTGTTTC 347
DB 302 ATCTTTTACTATCTATGAGTACTGGGTCACAGGAGTCAAGGACACAGTCAACCGTCTC 356

RESULT 11

US-08-672-176A-5
Sequence 5, Application US/08672176A
Patent No. 5908925

GENERAL INFORMATION:

APPLICANT: Cohen, Margo P.; Shearman, Clyde W.
TITLE OF INVENTION: Genetically Engineered Immunoglobulins with
TITLE OF INVENTION: Specificity for Glycosylated Albumin

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Exocell, Inc.

STREET: 3508 Market Street, suite 420

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19104

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette, 3.50 inch, 1.4 Mb storage

COMPUTER: PC

OPERATING SYSTEM: DOS 4.0 or better

SOFTWARE: Wordperfect, Version 5.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,176A

FILING DATE: unknown

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: N/A

FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Silver, Robert S.
REGISTRATION NUMBER: unknown
REFERENCE/DOCKET NUMBER: E1042/20002
TELEPHONE: 215-567-2010
TELEFAX: 215-751-1142
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs/240 amino acid residues
TYPE: nucleic acid/amino acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: humanized A717 immunoglobulin single-chain Fv
HYPOTHETICAL: yes
ANTI-SENSE: no
FRAGMENT TYPE: N-terminal fragment
ORIGINAL SOURCE: synthetic
ORGANISM: N/A
STRAIN: N/A
INDIVIDUAL ISOLATE: N/A
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: plasmid
LIBRARY: N/A
CLONE: pHuA717scfv-1
POSITION IN GENOME: N/A
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE: HuA717VH-1 linked to HuA717VL
NAME/KEY: HuA717VH; linker; HuA717VL
LOCATION: aa# 1-120; aa# 121-133; aa# 134-240
IDENTIFICATION METHOD: similarity to known sequences
OTHER INFORMATION: antigen is human glycosylated albumin
PUBLICATION INFORMATION: N/A
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5:
US-08-672-176A-5

Query Match 68.5%; Score 240.6; DB 2; Length 720;
Best Local Similarity 82.3%; Pred. No. 1.8e-71;
Matches 292; Conservative 0; Mismatches 54; Indels 9; Gaps 1;

QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
DB 2 AGGTGACGCTGTGGAGTCTGGGGAGGCGTGTGTCAGCCTGGAAGGTCCCTGAGACTCT 61
QY 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGTTGGGTTCGCCAGGCTC 121
DB 62 CCGTGCAGCCTCTGATTCACCTTCAGTAGCTATGACATGTTGGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
DB 122 CCGGCAAGGCTGTGAGTGGTTCGCAAAAGTTAGTAGTGGTGTGACACCTACTATT 181
QY 182 TAGACACTGTGACGGCCGATTCACCATCTCCAGAGACAATAGTAGAAGACCCCTATACC 241

Db 182 CAGACAGTGTGAAGGCCCGATTACCATCTCCAGACACAATTCGAAGAACACAGTTGTACC 241
QY 242 TCCAATGAACCTCTGTAGAGCGGAGGACACAGCCGTGTATTACTGTGAAGA------ 294
Db 242 TCCAATGAACCTCTGTAGAGCGGAGGACACAGCCGTGTATTACTGTGAAGAGATGTT 301
QY 295 --CAAACTACGCGAGTCTTGTCTTACTGGGCGCAAGGAGTACAGTACTGTTTC 347
Db 302 ATCTTTATTACTATGCTATGGACTACTGGGGTCAAGGAACACAGTACCGTCTC 356

RESULT 12
US-08-475-000-15
; Sequence 15, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
US-08-475-000-15

Query Match 68.3%; Score 239.8; DB 1; Length 357;
Best Local Similarity 82.2%; Pred. No. 2.4e-71;
Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTGAGCGCTGGAAGGTCCTTGTGAGACTCT 61
Db 2 AGGTGAAGTGTGGAGTCTGGGGAGTCTTAGTGAGGCGCTGGAGGTCCTTGTGAACTCT 61
QY 62 CTGTGACAGCTGTGAGTACCTTACCTAGTATGACATGCTTGGGGTTCGCCAGGCTC 121
Db 62 CTGTGACAGCTGTGAGTACCTTACCTAGTATGACATGCTTGGGGTTCGCCAGGCTC 121
QY 122 CGGGAAGGCTGTGGAGTGGTGGCGAAAGTAGTAGTGGTGTAGTACCTACTATT 181
Db 122 CGGGAAGGCTGTGGAGTGGTGGCGAAAGTAGTAGTGGTGTAGTACCTACTATT 181
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACACCCCTATACC 241

Db 182 CAGACAGTGTGAAGGGTGCATTACCGTCTCCAGACACAATCCCATGAGCAGCTGTACC 241
QY 242 TCCAATGAACCTCTGTAGAGCGGAGGACACAGCGTGTATTACTGTGAAGACA------ 296
Db 242 TCCAATGAAGCAGTCTGAGGTCTGAGGACAGCGCCTTGTATTACTGTGAAGATACGGGG 301
QY 297 -TAACACTACGCGAGTCTTGTCTTACTGGGCGCAAGGAGTACAGTACTGTTTCT 348
Db 302 CTGGTGACGCGCTGGTCTTCTTACTGGGCGCAAGGAGTCTGGTACAGTTTCT 354

RESULT 13
US-08-483-199-15
; Sequence 15, Application US/08483199
; Patent No. 5849877
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
US-08-483-199-15

Query Match 68.3%; Score 239.8; DB 2; Length 357;
Best Local Similarity 82.2%; Pred. No. 2.4e-71;
Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;
QY 2 AGGTGACAGTGTGGAGTCTGGGGAGGCGTGTGTGAGCGCTGGAAGGTCCTTGTGAGACTCT 61
Db 2 AGGTGAAGTGTGGAGTCTGGGGAGTCTTAGTGAGGCGCTGGAGGTCCTTGTGAACTCT 61
QY 62 CTGTGACAGCTGTGAGTACCTTACCTAGTATGACATGCTTGGGGTTCGCCAGGCTC 121
Db 62 CTGTGACAGCTGTGAGTACCTTACCTAGTATGACATGCTTGGGGTTCGCCAGGCTC 121
QY 122 CGGGAAGGCTGTGGAGTGGTGGCGAAAGTAGTAGTGGTGTAGTACCTACTATT 181
Db 122 CGGGAAGGCTGTGGAGTGGTGGCGAAAGTAGTAGTGGTGTAGTACCTACTATT 181
QY 182 TAGACACTGTGCAGGCGCGATTACCATCTCCAGAGACAATAGTAGAACACCCCTATACC 241

Db 182 CAGACAGTGTGAAGGCTGCATTCCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
QY 242 TCGAATGAACCTCTCTGAGAGCCGAGGACACACCCGCTGTATTACTGTGCAAGACA----- 296
Db 242 TCGAATGAGCAGTCTGAGGCTGAGGACACACGCCCTGTATTACTGTGCAAGATACGGGG 301
QY 297 -TAACCTACGGCAGTTTGTCTTACTGGGGCCAAAGGACTACAGTACTGTTTCT 348
Db 302 CTGGTGACGCCCTGGTTTGTCTTACTGGGGCCAAAGGACTCTGTGTACAGTTTCT 354

RESULT 14
US-08-484-508-15
; Sequence 15, Application US/08484508
; Patent No. 5948647
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,508
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0850.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 801-585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
US-08-484-508-15

Query Match 68.3%; Score 239.8; DB 2; Length 357;
Best Local Similarity 82.2%; Pred. No. 2.4e-71;
Matches 290; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 2 AGGTGAGCTGTGGAGTCTGGGGAGGCGTGTGTGAGCCTGGAAGGTCCTGAGACTCT 61
Db 2 AGGTGAAGCTGTGGAGTCTGGGGAGTCTGTAGTAGGCTGGAGGTCCTGAAACTCT 61
QY 62 CCGTGTGAGCCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121
Db 62 CCGTGTGAGCCTGTGATTCACCTTCAGTAGCTATGACATGCTTGGTTCGCCAGGCTC 121
QY 122 CGGGCAAGGCTGTGGAGTGGTGGCGAAAAGTTAGTGTGTGTGTAGTGTAGCAGCTACTATT 181
Db 122 CGGAGAGCGGCTGTGGAGTGGTGGCGAACCATTTAGTGTGTGTGTAGTGTGTGTATCTATC 181
QY 182 TAGACACTGTGCAGGCCCGATTACCATCTCCAGAGACAATAGTAAGAACACCCCTATACC 241

Db 182 CAGACAGTGTGAAGGCTGCATTCCACCGTCTCCAGAGACAATGCCATGAGCAGCCTGTACC 241
QY 242 TCGAATGAACCTCTCTGAGAGCCGAGGACACACCCGCTGTATTACTGTGCAAGACA----- 296
Db 242 TCGAATGAGCAGTCTGAGGCTGAGGACACACGCCCTGTATTACTGTGCAAGATACGGGG 301
QY 297 -TAACCTACGGCAGTTTGTCTTACTGGGGCCAAAGGACTACAGTACTGTTTCT 348
Db 302 CTGGTGACGCCCTGGTTTGTCTTACTGGGGCCAAAGGACTCTGTGTACAGTTTCT 354

RESULT 15
US-08-053-171-10
; Sequence 10, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..445
; OTHER INFORMATION: /standard_name= "Heavy Chain
; OTHER INFORMATION: V-region of BR55-2 Antibody in pVg-1c and pVg-3c"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..425
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..6
; OTHER INFORMATION: /standard_name= "Xba I restriction
; OTHER INFORMATION: site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 440..445
; OTHER INFORMATION: /standard_name= "Xba I restriction
; OTHER INFORMATION: site"
US-08-053-171-10

Query Match

67.9%; Score 238.2; DB 1; Length 445;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:56 ; Search time 23.47 Seconds
(without alignments)
338.491 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQLVESGGGVQPGKSLRL.....RHNYGSPAYWGQGTITVSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_56: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	507	82.3	119	2	S31108	Ig heavy chain - h
2	503	81.7	119	2	C36005	Ig heavy chain v r
3	503	81.7	119	2	S31107	Ig heavy chain - h
4	503	81.7	121	2	S36666	Ig heavy chain v r
5	503	81.7	127	2	S38489	Ig heavy chain - h
6	503	81.7	140	2	S31588	Ig heavy chain v r
7	502	81.5	140	2	S31686	Ig heavy chain v r
8	501	81.3	134	2	S31679	Ig heavy chain v r
9	500.5	81.2	122	2	E36005	Ig heavy chain v r
10	499	81.0	132	2	S31603	Ig heavy chain v r
11	498.5	80.9	122	2	S31117	Ig heavy chain - h
12	498.5	80.9	128	2	S48797	Ig heavy chain v r
13	498	80.8	121	2	G36005	Ig heavy chain v r
14	494	80.2	119	2	G36005	Ig heavy chain v r
15	494	80.2	119	2	F36005	Ig heavy chain v r
16	494	80.2	123	2	S31114	Ig heavy chain - h
17	494	80.2	138	2	S31666	Ig heavy chain v r
18	493.5	80.1	120	2	S48798	Ig heavy chain v r
19	492.5	80.0	114	2	S46392	Ig heavy chain v r
20	492	79.9	117	2	S78486	Ig heavy chain v r
21	492	79.9	160	2	S05271	Ig heavy chain pre
22	491.5	79.8	114	2	S46390	Ig heavy chain v r
23	490	79.5	121	2	I55673	Ig heavy chain - h
24	488.5	79.3	137	2	S31701	Ig heavy chain v r
25	487	79.1	134	2	S31699	Ig heavy chain v r
26	485.5	78.8	118	2	S31116	Ig heavy chain - h
27	485.5	78.8	140	2	S70442	Ig heavy chain pre
28	485	78.7	133	2	A49028	Ig heavy chain v r
29	485	78.7	143	2	S23624	Ig heavy chain v r

ALIGNMENTS

RESULT 1
S31108
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31108
R:Raphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31108
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <PAA>
A:Cross-references: EMBL:X62956
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 507; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 1.4e-39;
Matches 98; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
Qy 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDSWVRQAPGKGLWYAKVSSGGSTYY 60
Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWYSAISGGSGSTYY 60
Qy 61 LDTVGRTTISRDNSKNTLYLQMNSLRAEDTAVYCA--RHNYGSFAYWGQGTITVSS 117
Db 61 ADSVKGRTTISRDNSKNTLYLQMNSLRAEDTAVYCAKDRRLTGTFTDYGQGTITVSS 119
RESULT 2
C36005
Ig heavy chain v region (30p1) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C:Accession: C36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A:Reference number: A36005; MUID:90349571
A:Accession: C36005
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M18513
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```
Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 3.3e-39;
Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DQ 1 EVQLVESGGGLVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYY 60

QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYICARH-NYGS-FAYWGQTTVTSS 117
DQ 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYICAKDAGWGSGFDYWGQTLVTSS 119

RESULT 3
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAX>
A:Cross-references: EMBL:X62955
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 3.3e-39;
Matches 98; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DQ 1 EVQLVESGGGLVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYY 60

QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYICARHNYGS--FAYWGQTTVTSS 117
DQ 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYICAKDPCASYYFDYWGQTLVTSS 119

RESULT 4
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MAR>
A:Cross-references: EMBL:X61646; NID:G37688; PIDN:CAA43827.1; PID:gl335369
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.4e-39;
Matches 98; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY *1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
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Db 1 QVQLVQSGGQVQPGSRSLRSLCAASGFTFSYGMHWVRQAPGKGLWVAVTSYDGSNKYY 60
QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYICARHNT---GSFAYWGQTTVTVS 116
Db 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYICARTGYSSGSGFDYWGQTLVTVS 120
QY 117 S 117
Db 121 S 121

RESULT 5
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38489
R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from
A:Reference number: S38488
A:Accession: S38489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z3028; NID:G414025; PIDN:CAA80563.1; PID:G414026
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 127;
Best Local Similarity 77.2%; Pred. No. 3.6e-39;
Matches 98; Conservative 6; Mismatches 11; Indels 12; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRSLRSLCAASGFTFSYDMSWVRQAPGKGLWVAKVSSGGSTYY 60
DQ 1 QVQLVQSGGQVQPGSLRLSRLCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYY 60

QY 61 LDTVGQRTISRDNKNTLYLQMNLSRAEDTAVYICARH-----NYGSFAYWG 108
DQ 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYICAKGFPASDYDSSGYISFDYWG 120
QY 109 QGTTVT 115
DQ 121 QGTLVT 127

RESULT 6
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31585
A:Accession: S31588
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; PID:G30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      81.7%; Score 503; DB 2; Length 140;
Best Local Similarity 80.2%; Pred. No. 4e-39;
Matches 97; Conservative 11; Mismatches 9; Indels 4; Gaps 2;
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10

10

A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34024
C:Genetics:
A:Gene: GDB:IGH; IGHDY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 2.2e-38;
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

Qy 1 QVQLVESGGVVQPGSRSLRSCAASGFTSSYDMNWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVQLLEGGVLPQGGSLRSCAASGFTSSYAMSWVRQAPGKLEWVSAISGGSTYY 60

Qy 61 LDTVGRETISRDNKNTLYLQMSLRADTAIVYCARHNYGS--FAYWGQTTVTSS 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAKQNDWDFWPGQTLVTSS 119

RESULT 15

F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 1
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571
A:Accession: F36005
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34026
C:Genetics:
A:Gene: GDB:IGH; IGHDY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 494; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 2.2e-38;
Matches 98; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

Qy 1 QVQLVESGGVVQPGSRSLRSCAASGFTSSYDMNWVRQAPGKLEWVAKVSSGGSTYY 60
Db 1 QVQLVESGGVVQPGSRSLRSCAASGFTSSYAMHWVRQAPGKLEWVAISDGSKYY 60

Qy 61 LDTVGRETISRDNKNTLYLQMSLRADTAIVYCARHNYGSFAY--WGQTTVTSS 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDKASDAFDIWGQTTVTSS 119

Search completed: February 13, 2001, 09:04:13
Job time: 77 sec

THIS PAGE IS
REDACTED

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:21 ; Search time 14.89 seconds
(without alignments)
253.755 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQLVSGGGVQPGRLRL.....RHNYGSFAYWGQTTVTYSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481.5	78.2	122	1 HV3G_HUMAN	P01768 homo sapien
2	456	74.0	121	1 HV3J_HUMAN	P01771 homo sapien
3	453	73.5	119	1 HV3I_HUMAN	P01770 homo sapien
4	451.5	73.3	136	1 HV16_MOUSE	P01783 mus musculus
5	449.5	73.0	126	1 HV3K_HUMAN	P01772 homo sapien
6	446	72.4	117	1 HV3C_HUMAN	P01764 homo sapien
7	442.5	71.8	114	1 HV3B_HUMAN	P01763 homo sapien
8	441.5	71.7	116	1 HV3T_HUMAN	P01781 homo sapien
9	441.5	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
10	428	69.5	117	1 HV55_MOUSE	P01826 mus musculus
11	424	68.8	115	1 HV3F_HUMAN	P01767 homo sapien
12	423	68.7	119	1 HV3L_HUMAN	P01773 homo sapien
13	418.5	67.9	116	1 HV05_CARAU	P19181 carassius a
14	418	67.9	117	1 HV54_MOUSE	P18525 mus musculus
15	415.5	67.5	119	1 HV37_MOUSE	P01807 mus musculus
16	415.5	67.5	119	1 HV40_MOUSE	P01810 mus musculus
17	415	67.4	115	1 HV3D_HUMAN	P01765 homo sapien
18	415	67.4	120	1 HV3E_HUMAN	P01766 homo sapien
19	410.5	66.6	119	1 HV3M_HUMAN	P01774 homo sapien
20	408.5	66.3	119	1 HV3N_HUMAN	P01775 homo sapien
21	407.5	66.2	120	1 HV3O_HUMAN	P01782 homo sapien
22	407.5	66.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	406	65.9	117	1 HV02_CANFA	P01785 canis famil
24	405.5	65.8	114	1 HV01_CANFA	P01784 canis famil
25	404	65.6	115	1 HV32_MOUSE	P01801 mus musculus
26	403.5	65.5	119	1 HV38_MOUSE	P01808 mus musculus
27	402.5	65.3	122	1 HV20_MOUSE	P01789 mus musculus
28	402	65.3	113	1 HV30_MOUSE	P01799 mus musculus
29	400	64.9	142	1 HV01_RAT	P01805 rattus norv
30	399	64.8	118	1 HV39_MOUSE	P01809 mus musculus
31	397	64.4	113	1 HV27_MOUSE	P01796 mus musculus
32	396.5	64.4	97	1 HV56_MOUSE	P18527 mus musculus
33	395.5	64.2	111	1 HV35_MOUSE	P01804 mus musculus

ALIGNMENTS

RESULT 1

HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT NON_TER 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 78.2%; Score 481.5; DB 1; Length 122;
Best Local Similarity 74.6%; Pred. No. 8.9e-42;
Matches 91; Conservative 12; Mismatches 14; Indels 5; Gaps 1;

Qy 1 QVQLVSGGGVQPGRLRLSCAASGFTFSYDMSWVRQAPKGLWVAKVSSGGSTYY 60
Db 1 QVELVESGGGVVQPGRLRLSCAASGFTFSYAMHWVRQPPKGLWVAVISYGBBKYY 50
Qy 61 LDTVGRTTISRDNSKNTLYLQMSLRADETAVYYCARH-----NYGSFAYWGQTTVT 115
Db 61 ABSYKGRITISRDNSKNTLYLQMSLRADETAVYYCARDRPLYGBYRAFNWVGQTLTV 120
Qy 116 SS 117
Db 121 SS 122

RESULT 2

HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION HIL.
OS Homo sapiens (Human).

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KW Immunoglobulin V region.
FT MOD_RES 1 1
FT FT DISULFID 22 96
FT FT NON_TER 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;

Query Match 73.5%; Score 453; DB 1; Length 119;
Best Local Similarity 75.6%; Pred. No. 6.3e-39;
Matches 90; Conservative 18; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVPSGQGVQPGSRSLRSLSCAASGFTFSYDMSVWRQAPGKLEWAKVSSGGSTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVPSGQGVQPGSRSLRSLSCAASGFTFSRYTHWRQAPGKLEWAVMSYGBBKHY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LDTVQGRFTSRDNSKNTLYLQNSLRDAEDTAVYYCARHNYGS--FAYWGQGTITVTYSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVNGRFTSRDNSKNTLYLQNSLRDPAEDTAVYYCARIDRTAMFFAHQCGGLTIVTSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC F01783;
AT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N:A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K.; Milstein C.; Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RT Nature 265:299-304(1977).
RN [3]
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CC -----
CC EMBL; J00522; AADI5290.1; -.
CC FIR; A02066; GLMS21.
CC INTERPRO: IPR003006; -.
CC PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 16
FT CHAIN 17 136
FT DOMAIN 115 119
FT FT DISULFID 120 136
FT FT DISULFID 120 136
FT FT CONFLICT 75 78
FT FT CONFLICT 89 90
FT FT CONFLICT 115 115
FT FT CONFLICT 120 120
FT FT CONFLICT 136 136
FT NON_TER 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
IG HEAVY CHAIN V REGION MOPC 21.
D SEGMENT.
JH4 SEGMENT.
HYAD -> DYAH (IN REF. 2).
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).

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Query Match          73.0%; Score 449.5; DB 1; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.5e-38;
Matches 90; Conservative 10; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYDSMSVWRQAPGKLEWVAKVSSGGSTYY 60
DB 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYDSMSVWRQAPGKLEWVAKVSSGGSTYY 60
QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRAEDTAVYYCAR---HNYGSPA-----YWGQGT 111
DB 61 ADSVKGRTISRDNSKNTLYQMNSLRAEDTAVYYCAR---HNYGSPA-----YWGQGT 120
QY 112 TVTVSS 117;
DB 121 PVTYSS 126;

RESULT 6
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN P01764;
AC AC
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
SEQUENCE FROM N.A.
RX MEDLINE-81101090; PubMed-6450418;
RA Matthyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -;
DR EMBL; M35415; AAA58735.1; -;
DR PIR; A02047; H3HU26.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1
FT CHAIN 19
FT CHAIN 20, 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117
FT SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match          72.4%; Score 446; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.1e-38;
Matches 84; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGPGRSLRLSCAASGFTFSYDSMSVWRQAPGKLEWVAKVSSGGSTYY 60
DB 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSYDSMSVWRQAPGKLEWVAKVSSGGSTYY 79
QY 61 LDTVQGRFTISRDNSKNTLYQMNSLRAEDTAVYYCAR 98
DB 80 GDSVKGRFTISRDNSKNTLYQMNSLRAEDTAVYYCAR 117

RESULT 7
HV3B_HUMAN STANDARD; PRT; 114 AA.
ID HV3B_HUMAN P01763;
AC AC

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RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO502; HVM334.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;

Query Match 69.5%; Score 428; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 2e-36;
Matches 80; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQVSGGGVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSGGGSTYY 60
DB 20 EVQVSGGGLVPGGSLKSLCAASGFTSSYDMSVWRQTPKRLWVAIYSSGGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR 98
DB 80 PTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR 117

RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 68.8%; Score 424; DB 1; Length 115;
Best Local Similarity 69.2%; Pred. No. 4.9e-36;
Matches 81; Conservative 20; Mismatches 14; Indels 2; Gaps 2;

QY 1 QVQVSGGGVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSGGGSTYY 60
DB 1 EVQVETGGGLVPGGSLKSLCAASGFTSSYDMSVWRQAPGKALZWVSATYR-GGTTY 59

QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCARHNYGSFYAWGQGTITVTS 117
DB 60 ADSVGRFTISRDRSRVTLQMSLRADTAVYYCAR-DLAARLFSGKGTITVTS 115
RESULT 12
HV3L_HUMAN
ID HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
IgA1 protease, digestion, Fab and Fc fragments, and the complete
amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; A1HUBR.
DR HSSP; P01772; 2IG2.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 51 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 68.7%; Score 423; DB 1; Length 119;
Best Local Similarity 69.5%; Pred. No. 6.5e-36;
Matches 82; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

QY 1 QVQVSGGGVQPGSRSLRLSCAASGFTSSYDMSVWRQAPGKLEWAKVSGGGSTYY 60
DB 1 QVQVSGGGVQPGSRSLRLSCTSAFNLSDYAMHWVRQAPGKALZWVALISYGSSTYY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAVYYCAR--HNYGSFYAWGQGTITVTS 116
DB 61 ADSVGRFTISRDRSRVTLQMSLRADTAVYYCAKLIYAVAGTBFWVGQGTITVTS 118

RESULT 13
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
and family relationships of two genes and a pseudogene in a teleost
fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.

```
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 5A.
FT CHAIN 20 116
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 84
FT DOMAIN 85 116
FT DISULFID 41 114
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 67.9%; Score 418.5; DB 1; Length 116;
Best Local Similarity 83.7%; Pred No. 1.8e-35;
Matches 82; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYMSWVRQPPGKGLWVSIVYSGSTYY 78
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR 98
Db 79 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYICAR 116

RESULT 14
HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH17183 SUBFAMILY.
DR PIR: J070505; HVMS84.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 67.9%; Score 418; DB 1; Length 117;
Best Local Similarity 79.6%; Pred No. 2e-35;
Matches 78; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSYMSWVRQPPGKGLWVSIVYSGSTYY 79
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR 98
Db 80 PDKVGRFTISRDNKNTLYLQMSLRADTAIVYICAR 117
```

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RESULT 15
HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR: A02077; AVMSX4.
DR HSSP: P01810; 2FBJ.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig: 1.
KW Immunoglobulin V region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 67.5%; Score 415.5; DB 1; Length 119;
Best Local Similarity 65.3%; Pred No. 3.7e-35;
Matches 77; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60
Db 1 EVKLESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKGLEWICEINPDSTINY 60
QY 61 LDTVQGRFTISRDNKNTLYLQMSLRADTAIVYICAR-HNYGSFAYWGQGTFTVSS 117
Db 61 TPLSKDKFTISRDNKNTLYLQMSKVRSEDTALYTCARLHYGYAAYWGQGLTVTSA 118

Search completed: February 13, 2001, 09:23:11
Job time: 1190 sec
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NO SCALE DIVISION

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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:56 ; Search time 39.42 seconds
(without alignments)
347.877 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 616
Sequence: 1 QVQVSGGVQVQGRSLRL.....RHNYGSFYWGQTTVTSS 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	78.4	116	4 Q9UL93	Q9ul93 homo sapien
2	475	77.1	113	4 Q9UL90	Q9ul90 homo sapien
3	474	76.9	121	4 Q9UL71	Q9ul71 homo sapien
4	464.5	75.4	147	4 Q9Y509	Q9y509 homo sapien
5	460.5	74.8	118	4 Q9UL72	Q9ul72 homo sapien
6	460.5	74.8	122	4 Q9UL84	Q9ul84 homo sapien
7	458.5	74.4	118	4 Q9UL91	Q9ul91 homo sapien
8	419	68.0	131	4 Q9UL88	Q9ul88 homo sapien
9	414	67.2	95	4 Q9UL86	Q9ul86 homo sapien
10	403.5	65.5	298	11 Q9QYF0	Q9qyf0 mus musculu
11	403.5	65.5	437	11 Q9RIA4	Q9ria4 mus musculu
12	382.5	62.1	124	4 Q9UL92	Q9ul92 homo sapien
13	372	60.4	104	4 Q9UL87	Q9ul87 homo sapien
14	366	59.4	112	4 Q9UGP3	Q9ugp3 homo sapien
15	351.5	57.1	124	6 Q9N0W4	Q9n0w4 oryctolagus
16	349	56.7	125	4 Q9UL95	Q9ul95 homo sapien
17	348.5	56.6	124	6 Q9N0W6	Q9n0w6 oryctolagus
18	339	55.0	117	11 Q9QXE9	Q9qxe9 mus musculu
19	336.5	54.6	118	11 Q9Z1C4	Q9z1c4 mus musculu

20	333	54.1	117	11 Q9QXF0	Q9qxf0 mus musculu
21	331.5	53.8	116	4 Q9UL89	Q9ul89 homo sapien
22	325	52.8	119	4 Q9UL94	Q9ul94 homo sapien
23	317.5	51.5	109	11 Q9JL75	Q9jl75 mus musculu
24	312	50.6	119	4 Q9UL73	Q9ul73 homo sapien
25	307	49.8	157	4 Q9S978	Q9s978 homo sapien
26	306.5	49.8	110	11 Q9JL83	Q9jl83 mus musculu
27	306	49.7	150	4 Q9Y298	Q9y298 homo sapien
28	304.5	49.4	150	4 Q9S973	Q9s973 homo sapien
29	302	49.0	77	4 Q9Y741	Q9y741 homo sapien
30	297	48.2	109	11 Q9JL85	Q9jl85 mus musculu
31	296.5	48.1	110	11 Q9JL77	Q9jl77 mus musculu
32	292.5	47.5	114	11 Q9JL81	Q9jl81 mus musculu
33	292.5	47.5	122	4 Q9UL75	Q9ul75 homo sapien
34	292	47.4	82	4 Q9Y729	Q9y729 homo sapien
35	290.5	47.2	77	4 Q9Y726	Q9y726 homo sapien
36	290	47.1	117	11 Q9Z1C6	Q9z1c6 mus musculu
37	288	46.8	78	4 Q9Y730	Q9y730 homo sapien
38	286.5	46.5	77	4 Q9Y728	Q9y728 homo sapien
39	286	46.4	102	11 Q9JL79	Q9jl79 mus musculu
40	276.5	44.9	416	4 Q9NPP6	Q9npp6 homo sapien
41	274	44.5	79	4 Q9Y731	Q9y731 homo sapien
42	274	44.5	81	4 Q9Y719	Q9y719 homo sapien
43	268.5	43.6	86	4 Q9Y722	Q9y722 homo sapien
44	266	43.2	80	4 Q9Y735	Q9y735 homo sapien
45	265.5	43.1	82	4 Q9Y732	Q9y732 homo sapien

ALIGNMENTS

RESULT	1
Q9UL93	
ID	Q9UL93
AC	Q9UL93;
DT	01-MAY-2000 (TRENBLrel. 13, Created)
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE	01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; PubMed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035021; AAD56257.1; -
DR	INTERPRO; IPR003006; -
DR	PFAM; PF00047; 1g; 1.
FT	NON_TER 1 1
FT	NON_TER 116 116
SQ	SEQUENCE 116 AA; 12434 MW; ODA0348154DD5061 CRC64;
Query Match 78.4%; Score 483; DB 4; Length 116;	
Best Local Similarity 81.0%; Pred. No. 2.2e-43;	
Matches 94; Conservative 5; Mismatches 17; Indels 0; Gaps 0;	
QY	2 VQVSGGVQVQGRSLRLSCAAGFTSFSSYDMWVRQPGKLEWAKVSSGGSTYL 61
DB	1 VQVSGGVQVQGRSLRLSCAAGFTSFSSYDMWVRQPGKLEWAKVSSGGSTYL 60
QY	62 DTQGRFTISRDNSKNTLYLQMNLSRAEDTAVYICARHNYGSFYWGQTTVTSS 117
DB	61 DSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYICARHNYGSFYWGQTTVTSS 116
RESULT	2

Q9UL90
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1. 1
FT NON_TER 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 77.1%; Score 475; DB 4; Length 113;
Best Local Similarity 79.5%; Pred. No. 1.4e-42;
Matches 93; Conservative 6; Mismatches 14; Indels 4; Gaps 1;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAKYSSGGSTYY 60
DB 1 EVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAFRYDGSNKYY 60
QY 61 LDTVGRTISRDNKNTLYLQMSLRAEDTAVYICARHNTGSGFYAGQGT 117
DB 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYICAK----DLNYSQGTIVTVSS 113
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

RESULT 3
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1. 1
FT NON_TER 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
Query Match 76.9%; Score 474; DB 4; Length 121;
Best Local Similarity 76.0%; Pred. No. 2e-42;
Matches 92; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAKYSSGGSTYY 60
DB 1 EVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAFRYDGSNKYY 60
QY 61 LDTVGRTISRDNKNTLYLQMSLRAEDTAVYICARHNTGSGFYAGQGT 116
DB 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYICAKGVTTIYDRFDINGOGTMTVTS 120
QY 117 S 117
DB 121 S 121
RESULT 4
Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9607114; PubMed=7475288;
RA Cao J., Vesicic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -
DR HSP; P01772; 2FB4.
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;
Query Match 75.4%; Score 464.5; DB 4; Length 147;
Best Local Similarity 71.4%; Pred. No. 2.5e-41;
Matches 90; Conservative 9; Mismatches 18; Indels 9; Gaps 1;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAKYSSGGSTYY 60
DB 1 QVHLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLWVAFRYDGSNKYY 60
QY 61 LDTVGRTISRDNKNTLYLQMSLRAEDTAVYICARHNTGSGFYAGQGT 111
DB 61 AGSVKGRTISRDNKNTLYLQMSLRAEDTAVYICAKDNGYFDSVGYAGIDYWGQGT 120
QY 112 TVTVSS 117
DB 121 LVTYSS 126
RESULT 5
Q9UL72
ID Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX* MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -;
DR HSSP; P01772; 2F84.
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 118;
Best Local Similarity 78.2%; Pred. No. 5e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps 2;
QY 1 QVQVESGGVQVQPGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQVESGGVQVQPGSLRLSCAASGFTVSSNMVVRQAPGKGLVSVS-VTVSGGSYY 59
QY 61 LTVQGRFTISRDNSKNTLYLQMSLRADETAVYICARHNYGSFA--YWGQGTITVVS 117
Db 60 ADSVKGRTISRDNSKNTLYLQMSLRADETAFYICARDRFGEFLFDYWGQGTITVVS 118

RESULT 6
Q9UL84 PRELIMINARY; PRT; 122 AA.
ID Q9UL84;
AC Q9UL84;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -;
DR HSSP; P01772; 2F84.
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5.2e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;
QY 1 QVQVESGGVQVQPGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQVESGGVQVQPGSLRLSCAASGFTSNMGHVRQAPGKGLVWVAISNDGSKNEY 60
QY 61 LTVQGRFTISRDNSKNTLYLQMSLRADETAVYICARHNYGS----PAYWQGTITV 115
Db 61 ADSVKGRTIFRDNSKNMMDLQMSLRADETAVYICAKDERGLVCTYFDYWGQGTITV 120
QY 116 SS 117
Db 121 SS 122

Query Match 74.8%; Score 460.5; DB 4; Length 122;
Best Local Similarity 73.8%; Pred. No. 5.2e-41;
Matches 90; Conservative 10; Mismatches 17; Indels 5; Gaps 1;
QY 1 QVQVESGGVQVQPGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQVESGGVQVQPGSLRLSCAASGFTSNMGHVRQAPGKGLVWVAISNDGSKNEY 60
QY 61 LTVQGRFTISRDNSKNTLYLQMSLRADETAVYICARHNYGS----PAYWQGTITV 115
Db 61 ADSVKGRTIFRDNSKNMMDLQMSLRADETAVYICAKDERGLVCTYFDYWGQGTITV 120
QY 116 SS 117
Db 121 SS 122

RESULT 7
Q9UL91 PRELIMINARY; PRT; 118 AA.
ID Q9UL91;
AC Q9UL91;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 74.4%; Score 458.5; DB 4; Length 118;
Best Local Similarity 76.9%; Pred. No. 8.1e-41;
Matches 90; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
QY 1 QVQVESGGVQVQPGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
Db 1 EVQVESGGVQVQPGSLRLSCAASGFTFSYDMSVVRQAPGKGLVWAKVSSGGSTYY 60
QY 61 LTVQGRFTISRDNSKNTLYLQMSLRADETAVYICARHNYG-SFAYWQGTITVVS 116
Db 61 ADSVKGRTISRDNAKNSLYLQMSLRADETAVYICARSDSEAFDYGQGTITVVS 117

RESULT 8
Q9UL88 PRELIMINARY; PRT; 131 AA.
ID Q9UL88;
AC Q9UL88;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 68.0%; Score 419; DB 4; Length 131;
Best Local Similarity 65.6%; Pred. No. 1.3e-36;
Matches 86; Conservative 10; Mismatches 21; Indels 14; Gaps 2;

RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	fetus.";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
DR	ENBL; AF035022; AAD56258.1; -.	
DR	INTERPRO: IPR003006; -.	
DR	PFAM: PF00047; ig; 1.	
FT	NON_TER	1
FT	NON_TER	124
SQ	SEQUENCE	124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

SEQUENCE FROM N.A.
Zafitropoulos A., Kandilogiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
Krambovitis E.,
"Induction of somatic mutations in human B cells by in vitro

RI Annotation: -, -, -, -
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RR EMBL: AJ132560; CAB65078.1; -
 DR EMBL: AJ132560; CAB65078.1; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; ig; 1.
 DR PFAM: PF00047; ig; 1.
 FT NON_TER 1
 FT NON_TER 112
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;

[illegible]

J. Biol. Chem. 275:13668-13676(2000).
 DR EMBL; AF245503; AAF68450.1; -.
 LR NON_TER 1 124
 FT NON_TER 124 124
 SQ SEQUENCE 124 AA; 13476 MW; 96D2B29FE47C24C8 CRC64;

Search completed: February 13, 2001, 09:04:56
Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:51 ; Search time 26.34 Seconds
(without alignments)
151.886 Million cell updates/sec

Title: US-08-790-540A-2

Perfect score: 616

Sequence: 1 QVQLVSGGCVQPGKSLRL.....RHNGSFAYWGQCTTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_36:*
- 1: /SIDSL1/gcgdata/geneseq/geneseq/AA1980.DAT:*
 - 2: /SIDSL1/gcgdata/geneseq/geneseq/AA1981.DAT:*
 - 3: /SIDSL1/gcgdata/geneseq/geneseq/AA1982.DAT:*
 - 4: /SIDSL1/gcgdata/geneseq/geneseq/AA1983.DAT:*
 - 5: /SIDSL1/gcgdata/geneseq/geneseq/AA1984.DAT:*
 - 6: /SIDSL1/gcgdata/geneseq/geneseq/AA1985.DAT:*
 - 7: /SIDSL1/gcgdata/geneseq/geneseq/AA1986.DAT:*
 - 8: /SIDSL1/gcgdata/geneseq/geneseq/AA1987.DAT:*
 - 9: /SIDSL1/gcgdata/geneseq/geneseq/AA1988.DAT:*
 - 10: /SIDSL1/gcgdata/geneseq/geneseq/AA1989.DAT:*
 - 11: /SIDSL1/gcgdata/geneseq/geneseq/AA1990.DAT:*
 - 12: /SIDSL1/gcgdata/geneseq/geneseq/AA1991.DAT:*
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 - 18: /SIDSL1/gcgdata/geneseq/geneseq/AA1997.DAT:*
 - 19: /SIDSL1/gcgdata/geneseq/geneseq/AA1998.DAT:*
 - 20: /SIDSL1/gcgdata/geneseq/geneseq/AA1999.DAT:*
 - 21: /SIDSL1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	117	19 W76001	Vitaxin antibody h
2	552	89.6	117	19 W76003	LM609 antibody hea
3	539	87.5	117	18 W27526	Heavy chain variab
4	539	87.5	239	20 W73874	Human antiFc epsil
5	539	87.5	242	20 W73876	Human antiFc epsil
6	536	87.0	117	20 Y06381	Murine monoclonal
7	525	85.2	130	20 Y06379	Murine monoclonal
8	523.5	85.0	118	19 W57591	Chimeric antibody
9	523.5	85.0	118	19 W89636	Human antibody hea
10	523.5	85.0	118	21 Y77512	Peptide seq ID No:
11	523.5	85.0	137	19 W57603	Chimeric antibody
12	523.5	85.0	137	20 W89635	Human antibody hea

13	523.5	85.0	137	21 Y77514	Peptide encoded by
14	517.5	84.0	139	15 R52823	Humanised murine K
15	517.5	84.0	139	16 R70471	Humanised anti-KC-
16	517.5	84.0	240	20 Y02472	A single chain ant
17	517	83.9	121	20 W86122	Protein sequence o
18	509.5	82.7	139	18 W21652	Humanised reshaped
19	509	82.6	240	21 Y15124	Anti-human CTLA-4
20	509	82.6	240	21 Y15125	Anti-murine CTLA-4
21	508	82.5	121	20 W86120	Protein sequence o
22	508	82.5	138	21 Y32406	Mouse anti-verotox
23	505	82.0	113	19 W70621	Human consensus fr
24	505	82.0	113	19 Y82347	Human consensus se
25	503.5	81.7	443	18 W13564	Humanised anti-L-s
26	503	81.7	117	20 W86137	Protein sequence o
27	502	81.5	119	14 R32240	Humanised MAb hea
28	501.5	81.4	120	18 W27553	Human Ab heavy cha
29	501.5	81.4	281	18 W27560	Consensus single c
30	500.5	81.2	131	18 W13520	Anti-melanoma anti
31	500.5	81.2	143	21 Y82829	Human PTHrp monocl
32	500	81.2	117	19 W48866	Chimeric humanized
33	500	81.2	117	20 W86135	Protein sequence o
34	500	81.2	264	19 W73049	Humanised A33 scab
35	500	81.2	532	19 W73051	233dCH2.z chimeric
36	500	81.2	643	19 W73050	233g2C237Az chimer
37	497.5	80.8	122	15 R50311	Humanised heavy ch
38	497.5	80.8	122	15 R50315	Humanised heavy ch
39	497.5	80.8	143	21 Y82621	Human PTHrp monocl
40	496.5	80.6	118	18 W06208	Xenograft antibody
41	496.5	80.6	120	19 W23952	Chimeric humanised
42	496.5	80.6	240	19 W23954	Chimeric humanised
43	496	80.5	117	16 R79157	Human IgE receptor
44	496	80.5	119	13 R23739	Recombinant heavy
45	496	80.5	119	14 R41721	Aglycosylated anti

ALIGNMENTS

RESULT 1

ID	W76001	standard; Protein; 117 AA.
XX	W76001;	
AC	W76001;	
DT	02-NOV-1998	(first entry)
DE	Vitaxin antibody heavy chain variable region protein fragment.	
XX	Vitaxin; antibody; variable region; heavy chain; integrin;	
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;	
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;	
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;	
KW	macular degeneration; osteoporosis.	
XX	Mus sp.	
OS	Mus sp.	
XX	WO9833919-A2.	
XX	06-AUG-1998.	
PD	30-JAN-1998;	98WO-US01826.
XX	30-JAN-1997;	97US-0791391.
XX	(IXSY-) IXSYS INC.	
PA	Glaser SM, Huse WD;	
XX	WPI; 1998-437472/37.	
DR	N-PSDB; V49820.	
XX	Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3	
PT	integrin - and related antibodies based on murine monoclonal	

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis

PS Claim 1; Fig 1a; 129pp; English.

XX This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g. cancer,
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 100.0%; Score 616; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPKGLVWAKVSSGGSTYY 60
Db 1 qvqlvesgggvvqpgksrlslscasgftfssydmsswvrqapkglewakvssggstyy 60

QY 61 LDTVGRTISRDNSKNTLYIQMNSLRADTAVYICARHNYGSPAYWGQGTIVTVSS 117
Db 61 ldtvggrtisdnskntlyiqmnslnsraedtavyycarhnygsfaywgqgtltvtss 117

RESULT 2

W76003
ID W76003 standard; Protein; 117 AA.

XX AC W76003;

DT 02-NOV-1998 (first entry)

XX LM609 antibody heavy chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.

XX OS Mus sp.

XX PN W09833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI: 1998-437472/37.

XX DR N-PSDB; V49822.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis

XX Claim 43; Fig 2a; 129pp; English.

CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

Query Match 89.6%; Score 552; DB 19; Length 117;
Best Local Similarity 88.0%; Pred. No. 1.1e-43;
Matches 103; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPKGLVWAKVSSGGSTYY 60
Db 1 evqlvesgggvlvqpgksrlslscasgftfssydmsswvrqipeklewkvssggstyy 60

QY 61 LDTVGRTISRDNSKNTLYIQMNSLRADTAVYICARHNYGSPAYWGQGTIVTVSS 117
Db 61 ldtvggrtisdnskntlyiqmnslnsraedtavyycarhnygsfaywgqgtltvtss 117

RESULT 3

W27526
ID W27526 standard; Protein; 117 AA.

XX AC W27526;

DT 16-DEC-1997 (first entry)

XX Heavy chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX OS Homo sapiens.

XX PN JP09191886-A.

XX PD 29-JUL-1997.

XX PF 19-JAN-1996; 96JP-0024816.

XX PR 19-JAN-1996; 96JP-0024816.

XX PA (ASAK) ASAHI BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHIIN KK.

XX PA (TSUR/) TSURA T.

XX DR WPI: 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medicinally and have low

PT antigenicity in humans

XX Claim 2; Page 13; 26pp; Japanese.

XX The present sequence, the heavy chain variable region of the human
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric
CC or chimeric MAb can be used to treat or prevent diseases, has very
CC specifically allergies, associated with the receptor, and has very

CC low antigenicity in humans.

XX Sequence 117 AA;

Query Match 87.5%; Score 539; DB 18; Length 117;

Best Local Similarity 86.3%; Pred. No. 1.6e-42;

Matches 101; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAKVSSGGSTYY 60

DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAFISNRGGSTYY 60

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 61 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 117

RESULT 4

W73874
ID W73874 standard; Protein; 239 AA.

XX AC W73874;

XX DT 31-MAR-1999 (first entry)

XX DE Human antiFc epsilon RI alpha chain antibody #2.

XX KW AntiFc epsilon RI alpha chain antibody; antibody production; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..19

XX FT Protein /note= "signal peptide"

XX FT Protein /note= "mature protein"

XX PN JP11000174-A.

XX PD 06-JAN-1999.

XX PF 13-JUN-1997; 97JP-0171232.

XX PR 13-JUN-1997; 97JP-0171232.

XX PA (ASAK) ASahi BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHI KK.

XX PA (TSUR/) TSURA T.

XX DR WPI; 1999-124394/11.

XX DR N-PSDB; X01214.

XX PT Preparing an antibody Fab fragment using yeast - in high yield

XX PS Claim 6; Page 7; 13pp; Japanese.

XX CC This sequence represents a human antiFc epsilon RI alpha chain antibody,

CC produced using the method of the invention. The method is for preparing

CC an antibody Fab fragment using the yeast Pichia pastoris as the host

CC cell. The method can prepare an antibody Fab fragment cost efficiently

CC and in high yield.

XX SQ Sequence 239 AA;

Query Match 87.5%; Score 539; DB 20; Length 239;

Best Local Similarity 86.3%; Pred. No. 3.6e-42;

Matches 101; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAKVSSGGSTYY 60

DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAFISNRGGSTYY 60

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 61 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 117

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAKVSSGGSTYY 60

DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAFISNRGGSTYY 60

DB 20 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAFISNRGGSTYY 79

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 80 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 136

RESULT 5

W73876
ID W73876 standard; Protein; 242 AA.

XX AC W73876;

XX DT 31-MAR-1999 (first entry)

XX DE Human antiFc epsilon RI alpha chain antibody #4.

XX KW AntiFc epsilon RI alpha chain antibody; antibody production; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..22

XX FT Protein /note= "signal peptide"

XX FT Protein /note= "mature protein"

XX PN JP11000174-A.

XX PD 06-JAN-1999.

XX PF 13-JUN-1997; 97JP-0171232.

XX PR 13-JUN-1997; 97JP-0171232.

XX PA (ASAK) ASahi BREWERIES LTD.

XX PA (NIKK-) NIKKA WHISKEY KK.

XX PA (TORI) TORII YAKUHI KK.

XX PA (TSUR/) TSURA T.

XX DR WPI; 1999-124394/11.

XX DR N-PSDB; X01216.

XX PT Preparing an antibody Fab fragment using yeast - in high yield

XX PS Claim 6; Page 9-10; 13pp; Japanese.

XX CC This sequence represents a human antiFc epsilon RI alpha chain antibody,

CC produced using the method of the invention. The method is for preparing

CC an antibody Fab fragment using the yeast Pichia pastoris as the host

CC cell. The method can prepare an antibody Fab fragment cost efficiently

CC and in high yield.

XX SQ Sequence 242 AA;

Query Match 87.5%; Score 539; DB 20; Length 242;

Best Local Similarity 86.3%; Pred. No. 3.6e-42;

Matches 101; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAKVSSGGSTYY 60

DB 23 EVQLVESGGGVQPGGSLRLSCAASGFTFSYDMNWVRQAPGKGLVWAFISNRGGSTYY 82

QY 61 LDTVGRTISRDNKNTLYLQMNSLRADTAVYICARHNYGSFAYWGQGTIVTVSS 117

DB 83 PDTVGRFTISRDNKNTLYLQMNSLRADTAVYICARHNYGMDYWGQGTIVTVSS 139

RESULT 6

Y06381

ID Y06381 standard; Protein; 117 AA.

XX

PA (CHUS) CHUGAI SEIYAKU KK.
 XX Sato K, Tsunenari T;
 XX WPI: 2000-117115/10.
 XX
 XX Treatment of hypercalcaemic crisis with a substance inhibiting binding
 PT of parathyroid hormone related peptide to its receptor
 XX
 XX Example 4; Page 95-96; 120pp; Japanese.
 XX
 CC The invention relates to a method of treatment of hypercalcaemic crisis.
 CC A composition for the treatment of hypercalcaemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (hPTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypercalcaemic crisis, such as that associated with
 CC a malignant tumour.
 XX
 XX Sequence 118 AA;
 SQ

Query Match 85.0%; Score 523.5; DB 21; Length 118;
 Best Local Similarity 87.3%; Pred. No. 4.3e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKGLEWVAKVSSGGSTYY 60
 DB 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKGLEWVAKVSSGGSTYY 60
 QY 61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGS-FAYWGQGTFTVSS 117
 DB 61 pdsvkgrftisrdnsknltlylqmnsraedtavyycarqgtmttyfaywgqgtltvss 118

RESULT 11
 W57603
 ID W57603 standard; Protein; 137 AA.
 XX
 AC W57603;
 XX
 DT 03-SEP-1998 (first entry)
 XX
 DE Chimeric antibody fragment against hPTHrP SEQ ID NO:58.
 XX
 KW Chimeric; antibody; human parathormone related peptide; hPTHrP; mouse;
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphoemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised.
 XX
 OS Synthetic.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 XX
 PN WO9813388-A1.
 XX
 PD 02-APR-1998.
 XX
 PF 24-SEP-1997; 97WO-JP03382.
 XX
 PR 24-JUL-1997; 97JP-0214168.
 PR 26-SEP-1996; 96JP-0255196.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Sato K, Wakahara Y, Yabuta N;
 XX
 XX WPI: 1998-230640/20.
 DR N-PSDB; V24243.
 XX

PT New chimeric antibodies against human parathormone related
 PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 PT disorders caused by malignant neoplasm(s)
 XX
 XX Claim 60; Page 122-123; 182pp; Japanese.
 XX
 CC New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTHrP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a specifically claimed region of
 CC an antibody of the invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphoemia such as that due to
 CC pathogens or to vitamin D resistance.
 XX
 XX Sequence 137 AA;
 SQ

Query Match 85.0%; Score 523.5; DB 19; Length 137;
 Best Local Similarity 87.3%; Pred. No. 5.1e-41;
 Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;
 QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKGLEWVAKVSSGGSTYY 60
 DB 20 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMQSVWVROAPGKGLEWVAKVSSGGSTYY 79
 QY 61 LDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYICARHNYGS-FAYWGQGTFTVSS 117
 DB 80 pdsvkgrftisrdnsknltlylqmnsraedtavyycarqgtmttyfaywgqgtltvss 137

RESULT 12
 W89635
 ID W89635 standard; Protein; 137 AA.
 XX
 AC W89635;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE Human antibody heavy chain protein.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW inhibitor; humanised.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal
 FT Protein 20..137
 XX
 PN WO9851329-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 13-MAY-1998; 98WO-JP02116.
 XX
 PR 18-JUL-1997; 97JP-0194445.
 PR 15-MAY-1997; 97JP-0125505.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Ishii K, Sato K, Tunenari T;
 XX
 XX WPI: 1999-070101/06.
 DR N-PSDB; X00116.
 XX
 XX Inhibitors of binding of parathyroid hormone related peptide to its
 PT receptor - useful for, e.g. treatment of cachexia arising from

PT cancer or other diseases

PS Example 4; Page 83-84; 125pp; Japanese.

XX The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC cancer, thereby improving the quality of life of the patient. The
 CC present sequence represents a human antibody heavy chain from the
 CC present invention.

XX SQ Sequence 137 AA;

Query Match 85.0%; Score 523.5; DB 20; Length 137;

Best Local Similarity 87.3%; Pred. No. 5.1e-41;

Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60

Db 20 qvqlvesgggvvqpgksrlslrscasgftfssygmwvrqapkglewatissggstyy 79

QY 61 LDTVOGRTISRDNSKNTLYIQMNSLRRAEDTAVYYCAHNYGS-FAYWGQGTITVSS 117

Db 80 pdsvkgrftisrdnskntlyiqmnsraedtavyycarqgttmtfyaywggtltvss 137

RESULT 13

Y77514

ID Y77514 standard; Protein; 137 AA.

XX AC Y77514;

DT 26-APR-2000 (first entry)

XX DE Peptide encoded by DNA seq ID No: 58.

XX KW Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

XX OS Homo sapiens.

XX PN WO200000219-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-JP03433.

XX PR 26-JUN-1998; 98JP-0180143.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Tsunenari T;

XX XX WPI; 2000-117115/10.

DR DR N-PSDB; 258914.

XX PT Treatment of hypercalcemic crisis with a substance inhibiting binding
 of parathyroid hormone related peptide to its receptor

XX PS Example 4; Page 98-99; 120pp; Japanese.

XX The invention relates to a method of treatment of hypercalcemic crisis.
 CC A composition for the treatment of hypercalcemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypercalcemic crisis, such as that associated with
 CC a malignant tumour.

XX SQ Sequence 137 AA;

Query Match 85.0%; Score 523.5; DB 21; Length 137;

Best Local Similarity 87.3%; Pred. No. 5.1e-41;

Matches 103; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60

Db 20 qvqlvesgggvvqpgksrlslrscasgftfssygmwvrqapkglewatissggstyy 79

QY 61 LDTVOGRTISRDNSKNTLYIQMNSLRRAEDTAVYYCAHNYGS-FAYWGQGTITVSS 117

Db 80 pdsvkgrftisrdnskntlyiqmnsraedtavyycarqgttmtfyaywggtltvss 137

RESULT 14

R52823

ID R52823 standard; Protein; 139 AA.

XX AC R52823;

DT 25-JAN-1995 (first entry)

XX XX Humanised murine KC-4 immunoglobulin heavy chain V-region.

XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;

chimeric antibody; human mammary fat globule; human breast carcinoma;
 murine anti-HMFG monoclonal antibody KC-4; humanised analogue.

XX OS Chimeric Mus musculus.

XX OS Chimeric Homo sapiens.

XX PN WO9411509-A.

XX PD 26-MAY-1994.

XX PF 16-NOV-1993; 93WO-US11445.

XX PR 16-NOV-1992; 92US-0977696.

XX PR 30-SEP-1993; 93US-0129930.

XX PR 08-OCT-1993; 93US-0134346.

XX PA (CANC-) CANCER RES FUND CONTRA COSTA.

XX PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;

XX DR WPI; 1994-183510/22.

XX DR N-PSDB; Q62804.

XX PT New analogue peptide(s) comprising antibody variable regions -
 used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms

XX PS Example 75; Page 95; 109pp; English.

XX CC This sequence represents a humanised murine anti-human carcinoma
 CC KC-4 antibody heavy chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.

XX SQ Sequence 139 AA;

Query Match

Best Local Similarity 84.0%; Score 517.5; DB 15; Length 139;

Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKGLEWAKVSSGGSTYY 60

Db 20 eqvmvsgggivqpggslrlscasgftafssyamsvrqapkglewaessggnvay 79

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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:02:52 ; Search time 18.5 Seconds
(without alignments)
113.566 Million cell updates/sec

Title: US-08-790-540A-2
Perfect score: 636
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.5	84.0	139	1	US-08-129-930B-96
2	505	82.0	113	3	US-08-974-899-6
3	503.5	81.7	443	4	PCT-US96-13152-4
4	502.5	81.6	122	2	US-07-934-373C-21
5	502.5	81.6	122	3	US-08-437-642B-21
6	502.5	81.6	122	4	PCT-US93-07832-21
7	502	81.5	119	1	US-08-053-171-12
8	502	81.5	125	1	US-08-478-039-99
9	502	81.5	125	1	US-08-478-349A-99
10	500.5	81.2	131	3	US-08-983-607-28
11	497.5	80.8	122	4	PCT-US93-08435-12
12	497.5	80.8	122	4	PCT-US93-08435-43
13	496	80.5	119	1	US-07-988-925-11
14	496	80.5	119	2	US-08-362-780-11
15	495	80.4	119	1	US-08-331-388A-46
16	495	80.4	119	2	US-08-331-397B-46
17	495	80.4	119	2	US-08-759-804A-46
18	495	80.4	119	4	PCT-US94-07659-6
19	494.5	80.3	117	1	US-07-942-245-36
20	494.5	80.3	122	4	PCT-US93-08435-14
21	494	80.2	120	1	US-07-942-245-35
22	494	80.2	125	2	US-08-428-197-1
23	494	80.2	125	4	PCT-US93-10555-1
24	492.5	80.0	116	3	US-08-983-607-36
25	491	79.7	123	2	US-08-665-202-30
26	489.5	79.5	120	2	US-07-934-373C-4
27	489.5	79.5	120	3	US-08-437-642B-4
28	489	79.4	119	1	US-08-207-996-22

29	489	79.4	119	2	US-08-760-840A-22	Sequence 22, Appl
30	489	79.4	119	3	US-09-266-119-22	Sequence 22, Appl
31	489	79.4	120	2	US-08-428-197-20	Sequence 20, Appl
32	489	79.4	120	4	PCT-US93-10555-20	Sequence 20, Appl
33	487	79.1	117	2	US-08-652-558-44	Sequence 44, Appl
34	487	79.1	120	2	US-08-428-197-22	Sequence 22, Appl
35	487	79.1	120	4	PCT-US93-10555-22	Sequence 22, Appl
36	486	78.9	117	2	US-08-652-558-46	Sequence 46, Appl
37	486	78.9	117	3	US-08-983-607-46	Sequence 46, Appl
38	486	78.9	120	2	US-08-428-197-24	Sequence 24, Appl
39	486	78.9	120	2	US-08-428-197-26	Sequence 26, Appl
40	486	78.9	120	2	US-08-428-197-28	Sequence 28, Appl
41	486	78.9	120	4	PCT-US93-10555-24	Sequence 24, Appl
42	486	78.9	120	4	PCT-US93-10555-26	Sequence 26, Appl
43	486	78.9	120	4	PCT-US93-10555-28	Sequence 28, Appl
44	485.5	78.8	140	3	US-08-983-607-32	Sequence 32, Appl
45	484.5	78.7	135	4	PCT-US95-07302-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/POCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-96

Query Match 84.0%; Score 517.5; DB 1; Length 139;
Best Local Similarity 83.3%; Pred. No. 6.7e-46;
Matches 100; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60
Db 20 EVQVLESGLVQPGSLRLSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 79
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNYGS---FAYWGQGTIVTVSS 117
Db 80 QDTVTGRTTISRDNKNTLYLQMSLRADTAIVYICAREDYGIPAWFAYWGQGTIVTVSS 139

RESULT 2

US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-974-899-6

Query Match 82.0%; Score 505; DB 3; Length 113;
Best Local Similarity 83.8%; Pred. No. 9.9e-45;
Matches 98; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVQVLESGLVQPGSLRLSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNYGSFAYWGQGTIVTVSS 117
Db 61 ADSVKGRTTISRDNKNTLYLQMSLRADTAIVYICAR----GFDYWGQGTIVTVSS 113

RESULT 3

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 81.7%; Score 503.5; DB 4; Length 443;
Best Local Similarity 83.8%; Pred. No. 6.9e-44;
Matches 98; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRSLRSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 60
Db 1 EVQVLESGLVQPGSLRLSCAASGFTFSYDMSVWRQAPGKLEWVAKVSSGGSTYY 59
Qy 61 LDTVGRTTISRDNKNTLYLQMSLRADTAIVYICARHNYGSFAYWGQGTIVTVSS 117
Db 60 PDSVKGRTTISRDNKNTLYLQMSLRADTAIVYICARDYDGDYWGQGTIVTVSS 116

RESULT 4
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-21

Query Match 81.6%; Score 502.5; DB 2; Length 122;
Best Local Similarity 80.3%; Pred. No. 1.9e-44;
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGDGSTYY 60
QY 61 LPTVGRFTISRDNSKNTLYLQMSLRRAEDTAVYYCARHNY-----GSFAYWCGGTVTY 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADVKGRFTISRDNSKNTLYLQMSLRRAEDTAVYYCARGRVGYSLSGLYDYGQGLTVTV 120
QY 116 SS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 SS 122

RESULT 5
US-08-437-642B-21
Sequence 21, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-21

Query Match 81.6%; Score 502.5; DB 3; Length 122;
Best Local Similarity 80.3%; Pred. No. 1.9e-44;
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSYDMNWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSVISGDGSTYY 60
QY 61 LPTVGRFTISRDNSKNTLYLQMSLRRAEDTAVYYCARHNY-----GSFAYWCGGTVTY 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADVKGRFTISRDNSKNTLYLQMSLRRAEDTAVYYCARGRVGYSLSGLYDYGQGLTVTV 120
QY 116 SS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 SS 122

RESULT 6
PCT-US93-07832-21
Sequence 21, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:

REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-21

Query Match 81.6%; Score 502.5; DB 4; Length 122;
Best Local Similarity 80.3%; Pred No. 1.9e-44;
Matches 98; Conservative 7; Mismatches 12; Indels 5; Gaps 1;
QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRSLCAASGFTFSYAMSWVRQAPGKLEWVSVISGDSSTYY 60
QY 61 LDTVGRTISRDNKNTLYLQMSLRADTAIVYCARHNY-----GSFAYWGQGTIVTV 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCARGRVGLSGLDYWGQGTIVTV 120
QY 116 SS 117
Db 121 SS 122

RESULT 7

US-08-053-171-12
; Sequence 12, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Sequence of Humanized

; Patent No. 5562903
; OTHER INFORMATION: BR55-2 Antibody, Heavy Chain Variant
; OTHER INFORMATION: H-hu-BR55-2/1"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 31..35
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 50..66
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 99..108
; OTHER INFORMATION: /note= "Complementarity-determining
; OTHER INFORMATION: region"
; US-08-053-171-12

Query Match 81.5%; Score 502; DB 1; Length 119;
Best Local Similarity 81.5%; Pred No. 2.1e-44;
Matches 97; Conservative 13; Mismatches 7; Indels 2; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRSLCAASGFTFSYDMSWVRQAPGKLEWAKVSSGGSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGKSLRSLCAASGFTFSYDMYWRQAPGKLEWVAYISNGGSSHY 60
QY 61 LDTVGRTISRDNKNTLYLQMSLRADTAIVYCAR-HNYGS-FAYWGQGTIVTVSS 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VDSVKGRTISRDNKNTLYLQMSLRADTAIVYCARGMIDYGAWFAYWGQGTIVTVSS 119

RESULT 8

US-08-478-039-99
; Sequence 99, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raad, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99

Query Match 81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.2e-44;
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
DB 1 EYQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVYXISGGSTYY 60
QY 61 LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHN---YGSFAY-----WQGGTT 112
DB 61 ADSVKGRTFISRDNSKNTLYLQMSLRAEDTAVYYCAKGVLYIGSGSYHWDFPWQGGTL 120
QY 113 VTVSS 117
DB 121 VTVSS 125

RESULT 9
US-08-476-349A-99
Sequence 99, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: Teskit Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-476-349A-99

Query Match 81.5%; Score 502; DB 1; Length 125;
Best Local Similarity 79.2%; Pred. No. 2.2e-44;
Matches 99; Conservative 8; Mismatches 10; Indels 8; Gaps 2;
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKLEWVAKVSSGGSTYY 60
DB 1 EYQLVESGGGLVQPGKSLRLSCAASGFTFSYAMSWVRQAPGKLEWVYXISGGSTYY 60
QY 61 LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYYCARHN---YGSFAY-----WQGGTT 112
DB 61 ADSVKGRTFISRDNSKNTLYLQMSLRAEDTAVYYCAKGVLYIGSGSYHWDFPWQGGTL 120
QY 113 VTVSS 117
DB 121 VTVSS 125

RESULT 10
US-08-983-607-28
Sequence 28, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544

```

/ RESCUE RUN polyptace
/
/ ORIGINAL SOURCE: Homo sapiens (melanoma patient immu-
/ ORGANISM: nized with autologous tumor cells)
/ ORGANISM: peripheral blood lymphocytes
/ INDIVIDUAL ISOLATE:
/ IMMEDIATE SOURCE:
/ LIBRARY: DM14 scfv antibodies obtained from
/ LIBRARY: FUSE5 fusion phage construct
/ CLONE: V13
/ FEATURE:
/ NAME/KEY: heavy chain
/ US-08-983-607-28

```

```
Query Match      80.8%; Score 497.5; DB.4; Length 122;
Best Local Similarity 79.5%; Pred. No. 6.3e-44;
Matches 97; Conservative 9; Mismatches 11; Indels 5
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61	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
62	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
63	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
64	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
65	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
66	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
67	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
68	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
69	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
70	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
71	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
72	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S	T	Y	60
73	QY	1	QV	LV	ES	GGG	V	Q	R	S	L	R	L	S	C	A	S	G	T	T	S	S	D	K	S	W	R	A	P	K	G	L	E	W	A	K	S	S	G	G	S			

RESULT 12
PCT-US93-08435-43
; Sequence 43, Application PC/TUS9308435

; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham, Corporation
 ; APPLICANT: U. S. Government, Secretary of
 ; APPLICANT: the Navy
 ; APPLICANT: U. S. Government, Secretary of
 ; APPLICANT: the Army

TITLE OF INVENTION: Novel Antibodies for Conferring Passive
 TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Box 457, 321 Norristown Road
 CITY: Spring House
 STATE: PA
 COUNTRY: USA
 ZIP: 19477

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FILING DATE: .
CLASSIFICATION:

PRIOR APPLICATION DATA: US 07/941,654
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-43

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Db      1  EVQLLESQGLVPGGSLRLSCAASGTTFFSFPMVAVRQAPGKLEWVSTISTSGRTYY 6
QY      61  LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYICA--RHNYGSPAYWGQGTFTTVSS 117
           1:|||||
Db      61  RDSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICAKFRQYSGGFDYWGQGTFLTVSS 119
           1:|||||

RESULT 14
US-08-362-780-11
; Sequence 11, Application US/08362780
; Patent No. 5968509
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D
; APPLICANT: Routledge, Edward G
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: Antibody Preparation
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye PC
; STREET: 8th Floor, 1100 No. 5968509th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119-amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-362-780-11

Query Match: 80.5%; Score 496; DB 2; Length 119;
Best Local Similarity 79.8%; Pred. No. 8.7e-44;
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps

QY      1  QQLVESGGGVVPGGSLRLSCAASGTTFFSYDMSVWRQAPGKLEWAVKSVSGGSGTYY 60
           1:|||||
Db      1  EVQLLESQGLVPGGSLRLSCAASGTTFFSFPMVAVRQAPGKLEWVSTISTSGRTYY 60
           1:|||||

QY      61  LDTVQGRFTISRDNSKNTLYLQMSLRAEDTAVYICA--RHNYGSPAYWGQGTFTTVSS 117
           1:|||||
Db      61  RDSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICAKFRQYSGGFDYWGQGTFLTVSS 119
           1:|||||

RESULT 15
US-08-331-398A-46
; Sequence 46, Application US/08331398A

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:13:00 ; Search time 1535.21 Seconds
(without alignments)
1070.080 Million cell updates/sec

Title: US-08-790-540A-3
Perfect score: 321
Sequence: 1 GAGATTGCTACTACTCAGTC.....GGACCAAGGTGGAANTTAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_bal.*
- 2: gb_ba2.*
- 3: gb_on.*
- 4: gb_ov.*
- 5: gb_ph.*
- 6: gb_pl1.*
- 7: gb_pl2.*
- 8: gb_pr1.*
- 9: gb_pr2.*
- 10: gb_pr3.*
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- 65: gb_htg18.*
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- 73: gb_ba3.*
- 74: em_htg8.*
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- 76: em_htg10.*
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- 78: gb_pr7.*
- 79: gb_sts1.*
- 80: gb_sts2.*
- 81: gb_pat1.*
- 82: gb_pat2.*
- 83: em_htg0.*
- 84: gb_htg24.*
- 85: gb_pr8.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	247.2	77.0	321	11	MUSCMVF
2	247.2	77.0	321	11	MUSIGKACY
3	247.2	77.0	370	11	MUSIGKXD
4	245.6	76.5	321	11	AF163757
5	245.6	76.5	321	11	MUSCMVH
6	245.6	76.5	381	81	E07933
7	245.6	76.5	381	81	I31959
8	245.6	76.5	381	82	I78571
9	245.6	76.5	381	82	I78626
10	245.6	76.5	431	11	MUSIGKCNJ
11	244.4	76.1	324	11	AF139844
12	244.4	76.0	324	11	AF139849
13	244.4	76.0	330	11	MUSIGL2VK
14	242.4	75.5	324	11	AF139845
15	242.4	75.5	324	11	AF139846
16	242.4	75.5	381	11	AF045514
17	242.4	75.5	582	11	MMU26998
18	242.4	75.5	738	11	MMU40581
19	240.8	75.0	321	11	AF13242
20	240.8	75.0	321	11	AF13243
21	240.8	75.0	321	11	MMU27215

22 240.8 75.0 321 11 MMU277216
23 240.8 75.0 324 11 AF139847
24 240.8 75.0 324 11 AF139848
25 240.8 75.0 348 11 MMY16070
26 240.4 74.9 324 11 MMU60469
27 239.6 74.6 420 11 MUSIGKCKN
28 239.6 74.6 5238 81 AF07699
29 239.2 74.5 324 11 AF087031
30 238.6 74.3 317 11 MMIGIKL4
31 238 74.1 317 11 MMIGIKL3
32 235 73.2 313 11 MUSIGVABU
33 234.6 73.1 321 11 MMU16181
34 234.4 73.0 381 11 MUSIGKAQA
35 234.2 73.0 307 11 AF139235
36 234 72.9 313 11 MUSIGVABW
37 233.8 72.8 318 11 MMIGKVR4
38 233.6 72.8 323 11 MMU2NDNF
39 233.2 72.6 306 11 MMIGLT91
40 233.2 72.6 315 11 MMU88691
41 232.8 72.5 300 11 MUSIGKABY
42 232.8 72.5 321 11 MMALCVR26
43 232 72.3 318 11 MMU88689
44 231.2 72.0 324 11 MMU16184
45 230.2 71.7 303 11 S66242

ALIGNMENTS

RESULT 1
MUSCMVF MUSCMVF 321 bp mRNA ROD 26-JUL-1993
DEFINITION Mouse mRNA sequence, partial cds.
ACCESSION M95943
VERSION M95943.1 GI:309175
KEYWORDS
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
Co.M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
TITLE Unpublished (1992)
JOURNAL
FEATURES
Location/Qualifiers
source 1..321
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="Mab 33"
/cell_type="hybridoma"

mat_peptide 85 a 81 c 74 g 80 t
BASE COUNT 85 a 81 c 74 g 80 t
ORIGIN

Query Match 77.0%; Score 247.2; DB 11; Length 321;
Best Local Similarity 85.3%; Pred. NO. 2.le-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;
QY 1 GAGATTGCTCAACTCTCCAGCCACCCTCTCTCAGCCAGGAGAGGCGACT 60
DB 1 GATATTGCTCAACTCAGTCTCCAGCCACCCTCTCTGCTGACTCCAGGAGATCGCTCAGT 60
QY 61 CTTTCCTGCGAGCCAGGCAAGATTATAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 61 CTTTCCTGCGAGCCAGGCAAGATTATAGCAACACCTACACTGCTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180

DB 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCCAAGTCCATCTCTGGGATCCCTCC 180
QY 181 AGGTTCACTGCGAGTGGATCAGGACAGATTTCACCTCTCATCTCTCCAGCTCTGGAGCT 240
DB 181 AGGTTCACTGCGAGTGGTTCAGGACAGATTTCACCTCTCATCTATCAACAGTGTGGAGACT 240
QY 241 GAAGATTGTCAGTCTATCTACTGTCAACAGAGTGGCAGCTGGCCTCAACACGTTGGAGGG 300
DB 241 GAAGATTGTCAGTCTATCTTGTCTCAACAGACTAACAGTGGCCTCATACGTTGGGGGG 300
QY 301 GGGACCAAGTGGAAATTA 320
DB 301 GGGACCAAGTGGAAATTA 320
RESULT 2
MUSIGKACY MUSIGKACY 321 bp mRNA ROD 27-APR-1993
LOCUS Mouse lysozyme-binding Ig kappa chain (HyHEL-10) V23-J2 region
DEFINITION mRNA, partial cds.
ACCESSION M35667
VERSION M35667.1 GI:196584
KEYWORDS immunoglobulin light chain; immunoglobulin-kappa; processed gene;
variable region VK23.
SOURCE Mouse hybridoma, CDNA to mRNA, clone 10K-106.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Mainhart, S.-G.-S.J., Lavoie, C., Feldman, T.B., Drohan, R.J. and
Brooks, W.B.R.
TITLE A three-dimensional model of an anti-lysozyme antibody
JOURNAL J. Mol. Biol. 194, 713-724 (1987)
MEDLINE 88011212
FEATURES
Location/Qualifiers
source 1..321
/organism="Mus musculus"
/db_xref="taxon:10090"
/note="lysozyme binding Ig kappa chain V23-J2 region"
/codon_start=1
/protein_id="AAA38741.1"
/db_xref="GI:196585"
/translation="DIVLTQSPATLSVTPGNSVLSQASQSGINLNHWYQOKSHESP
RLIKVASQSIGIPSRFSGSGSDFTLSINVTEDFGMYFCQSNWPYTFGGT
KLEIK"

BASE COUNT 88 a 80 c 75 g 78 t
ORIGIN

Query Match 77.0%; Score 247.2; DB 11; Length 321;
Best Local Similarity 85.3%; Pred. NO. 2.le-64;
Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGCTCAACTCAGTCTCCAGCCACCCTCTCTCAGCCAGGAGAGGCGACT 60
DB 1 GATATTGCTCAACTCAGTCTCCAGCCACCCTCTCTGCTGACTCCAGGAAATAGGCTCAGT 60
QY 61 CTTTCCTGCGAGCCAGGCAAGATTATAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 61 CTTTCCTGCGAGCCAGGCAAGATTATAGCAACACCTACACTGCTATCAACAAGGCGCT 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
DB 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCCAAGTCCATCTCTGGGATCCCTCC 180
QY 181 AGGTTCACTGCGAGTGGATCAGGACAGATTTCACCTCTCATCTCTCCAGCTCTGGAGCT 240
DB 181 AGGTTCACTGCGAGTGGATCAGGACAGATTTCACCTCTCATCTCAACAGTGTGGAGACT 240
QY 241 GAAGATTGTCAGTCTATCTACTGTCAACAGAGTGGCAGCTGGCCTCAACACGTTGGAGGG 300
DB 241 GAAGATTGTCAGTCTATCTTGTCTCAACAGAGTAACAGTGGCGCTACACGTTGGAGGG 300

QY 301 GGGACCAAGGTGGAATAA 320
|||||
Db 301 GGGACCAAGGTGGAATAA 320

RESULT 3

MUSIGKXD 370 bp mRNA ROD 27-APR-1993
LOCUS Mouse Ig active kappa-chain V-region, partial cds.
DEFINITION M93959
ACCESSION M93959
VERSION M93959.1 GI:197572
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 370)
AUTHORS Takeda, Y., Wise, K.S. and Hoffman, R.W.
TITLE Nucleotide sequences of immunoglobulin heavy and light chain
V-regions from a monoclonal autoantibody specific for a unique set
of small nuclear ribonucleoprotein complexes

JOURNAL Nucleic Acids Res. 20, 4099-4099 (1992)

MEDLINE 92375706

FEATURES Location/Qualifiers

1..370 /organism="Mus musculus"

/db_xref="taxon:10090"

/map="6"

1..370 /gene="Igk"

1..370 /partial

/gene="Igk"

/note="putative"

/codon_start=1

/function="variable region"

/product="immunoglobulin kappa-chain"

/protein_id="AAA39079.1"

/db_xref="GI:554148"

/translation="GLMLFWSASRGDIVLTQSPATLSVTPGDVSLSCRASQISNY
LHWYQKSHESPRLLIKYVSIGIPSRFSGSGDTFTLSINSVETEDFGMYFCQQ
SNSWPHFGSGTKLEIKRADA"

BASE COUNT 96 a 90 c 86 g 98 t

ORIGIN

Query Match 77.0%; Score 247.2; DB 11; Length 370;

Best Local Similarity 85.3%; Pred. No. 2.1e-64;

Matches 273; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

Db 37 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAAGTCAGT 96

QY 61 CTTTCTCTGCAGGCGAGCAAAAGTATTAGCAACCACTACCTGCTATCAACAAAGGCCT 120

Db 97 CTTTCTCTGCAGGCGAGCAAAAGTATTAGCAACCACTACCTGCTATCAACAAATCA 156

QY 121 GGTCAAGCCCCAAGGCTTCTATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGCC 180

Db 157 CATGAGTCTCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 216

QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCAGTCTCCAGTCTGGAGCCT 240

Db 217 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCTCTCAGTATCAACAGTGTGGAGCT 276

QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300

Db 277 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 336

QY 301 GGGACCAAGGTGGAATAA 320

Db 337 GGGACCAAGCTGGAATAA 356
|||||

RESULT 4

AF163757 321 bp mRNA ROD 04-AUG-1999
LOCUS Mus musculus mab 101.4.1 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.

ACCESSION AF163757

VERSION AF163757.1 GI:5690320

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 321)

AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.

TITLE Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal

Mouse Monoclonal Antibodies

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 321)

AUTHORS Mertens, N.M. and Cunningham, M.W.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma

University Health Sciences Center, 940 St. Young Blvd, Oklahoma

City, OK 73190, USA

FEATURES Location/Qualifiers

1..321 /organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/note="mab 101.4.1"

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/codon_start=1

/product="immunoglobulin light chain variable region"

/protein_id="AAD47036.1"

/db_xref="GI:5690321"

/translation="DIVLTQSPATLSVTPGDSVLSCLSRASQISNNLHWYQKSHESP

RLLIKVASQISIGIPSRFSGSGDTFTLSINSVETEDFGMYFCQSNLWTFGAGT

KLEIK"

BASE COUNT 83 a 83 c 73 g 82 t

ORIGIN

Query Match 76.5%; Score 245.6; DB 11; Length 321;

Best Local Similarity 85.0%; Pred. No. 6.4e-64;

Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60

Db 1 GATATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGCTCAGT 60

QY 61 CTTTCTCTGCAGGCGAGCAAAAGTATTAGCAACCACTACCTGCTATCAACAAAGGCCT 120

Db 61 CTTTCTCTGCAGGCGAGCAAAAGTATTAGCAACCACTACCTGCTATCAACAAATCA 120

QY 121 GGTCAAGCCCCAAGGCTTCTATCMKKTATCGTCCAGTCCATCTCTGGGATCCCGCC 180

Db 121 CATGAGTCTCCAAGGCTTCTATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 180

QY 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCCCTCAGTCTCCAGTCTGGAGCCT 240

Db 181 AGGTTTCAGTGGCAGTGGATCAGGACAGATTTACCTCTCAGTATCAACAGTGTGGAGCT 240

QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300

Db 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGGCAGTGGCCTCACACGTTTCGAGGG 300

QY 301 GGGACCAAGGTGGAATAA 320

|||||

Db 301 GGGACCAAGGTGGAATAA 320

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RESULT 5
MUSCMVH      MUSCMVH      321 bp      mRNA      ROD      26-JUL-1993
LOCUS
DEFINITION   Mouse mRNA sequence, partial cds.
ACCESSION   M95945
VERSION      M95945.1 GI:309177
KEYWORDS
SOURCE
ORGANISM     Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
              Simpson, J.A., Chow, J.C., Baker, J., Avdalovic, N.M., Yuan, S.,
              Co.M.S., Vasquez, M., Britt, W.J. and Coelingh, K.L.
TITLE
JOURNAL      Untitled
FEATURES
source       Location/Qualifiers
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              /sub_species="domesticus"
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              /cell_line="MAB 5"
              /cell_type="hybridoma"
              1..321
              /note="putative"
BASE COUNT   85 a 79 c 77 g 80 t
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Query Match      76.5%; Score 245.6; DB 11; Length 321;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGAAAGGGGACT 60
   |||
DB 1 GATATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGATAGCGTCACT 60
   |||

QY 61 CTTTCTGCGAGCGGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
   |||
DB 61 CTTTCTGCGAGCGGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
   |||

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
   |||
DB 121 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 180
   |||

QY 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
   |||
DB 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCTCTCAAGTCTGGAGACT 240
   |||

QY 241 GAAGATTTGCGAGTCTATTACTGTCAACAGAGTGGCGCTGCCCTCACAGTTCCGAGGG 300
   |||
DB 241 GAAGATTTGCGAGTCTATTCTGTCAACAGAGTAAAGTGGCCTCATACAGTTCCGAGGG 300
   |||

QY 301 GGGACCAAGGTGGAAATTA 320
   |||
DB 301 GGGACCAAGCTGGAGCTGNA 380
   |||

RESULT 6
E07933      E07933      381 bp      RNA      PAT      29-SEP-1997
LOCUS
DEFINITION   CDNA encoding variable region of mouse anti-FHV-1 antibody L chain.
ACCESSION   E07933
VERSION      E07933.1 GI:2176065
KEYWORDS
SOURCE      Mus sp.
ORGANISM     Mus sp.
              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
              Rodentia; Sclurognathi; Muridae; Murinae; Mus.
              Kurumi.K., Maeda.H., Nishiyama.K. and Tokiyoshi.Y.
REFERENCE    1 (bases 1 to 381)
AUTHORS      Kurumi.K., Maeda.H., Nishiyama.K. and Tokiyoshi.Y.

TITLE
JOURNAL
FEATURES
source       Location/Qualifiers
              1..381
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              /db_xref="taxon:10095"
BASE COUNT   94 a 98 c 86 g 103 t
ORIGIN

Query Match      76.5%; Score 245.6; DB 81; Length 381;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGTCTAAGTCTCCAGCCACCCCTGTCTCTCAGCCCGAGGAGAAAGGGGACT 60
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DB 61 GATATTGTCTAAGTCTCCAGCCACCCCTGTCTGTGACTCCAGGAGATAGCGTCACT 120
   |||

QY 61 CTTTCTGCGAGCGGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
   |||
DB 121 CTTTCTGCGAGCGGCAAGATATTAGCAACCACTACACTGGTATCAACAAGGCGCT 120
   |||

QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
   |||
DB 181 CATGAGTCTCCAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGCC 240
   |||

QY 181 AGGTTTCAGTGGGATCGAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
   |||
DB 241 AGGTTTCAGTGGGATCGAGGACAGATTTCACTCTCAAGTCTGGAGACT 300
   |||

QY 241 GAAGATTTGCGAGTCTATTACTGTCAACAGAGTGGCGCTGCCCTCACAGTTCCGAGGG 300
   |||
DB 301 GAAGATTTGCGAGTCTATTCTGTCAACAGAGTAAAGTGGCCTCATACAGTTCCGAGGG 360
   |||

QY 301 GGGACCAAGGTGGAAATTA 320
   |||
DB 361 GGGACCAAGCTGGAGCTGNA 380
   |||

RESULT 7
I31959      I31959      381 bp      DNA      PAT      06-FEB-1997
LOCUS
DEFINITION   Sequence .82 from patent US 5585089.
ACCESSION   I31959
VERSION      I31959.1 GI:1822750
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
              Unclassified.
              1 (bases 1 to 381)
              Queen,C.I. and Selick,H.E.
              Humanized immunoglobulins
REFERENCE    1 (bases 1 to 381)
AUTHORS      Queen,C.I. and Selick,H.E.
TITLE
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SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL Rule, G.S.
REFERENCE 1 (bases 1 to 56)
AUTHORS Unpublished (1988)
TITLE Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
MEDLINE 88234486
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
G. Rule, 20-JUL-1988
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source Location/Qualifiers
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/sub_species="domesticus"
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/cell_type="mature B cell"
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/db_xref="GI:197034"
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FGMYFCQSQNSWPTFGGKLEIKRADAAP"
93..431
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BASE COUNT 113 a 107 c 102 g 109 t
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Query Match 76.5%; Score 245.6; DB 11; Length 431;
Best Local Similarity 85.0%; Pred. No. 6.4e-64;
Matches 272; Conservative 2; Mismatches 45; Indels 0; Gaps 0;
Qy 1 GAGATTGTGCTAAGTCTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
Db 93 GATATTGTGCTAAGTCTCTCCAGCCACCTGTCTGTGACTCCAGGAGATAGCTCAGT 152
Qy 61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 120
Db 153 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 212
Qy 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
Db 213 CATGAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 272
Qy 181 AGTTTCAGTGGCAGTGGATGATGAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCT 240
Db 273 AGTTTCAGTGGCAGTGGATGATGAGGACAGATTTCACCTCACTATCTCCAGTCTGGAGCT 332
Qy 241 GAAGATTTTGAGTCTATATCTGTCACAGAGTGGCAGTGGCTGCACAGCTTCGGAGGG 300
Db 333 GAAGATTTTGAGTCTATATCTGTCACAGAGTGGCAGTGGCTGCACAGCTTCGGAGGG 392
Qy 301 GGGACCAAGGTGGAATTA 320
Db 393 GGGACCAAGGTGGAATTA 412
RESULT 11
AF139844 324 bp mRNA ROD 04-NOV-1999
LOCUS AF139844
DEFINITION Mus musculus clone 50 immunoglobulin kappa light chain variable
region VK23 (196) mRNA, partial cds.
ACCESSION AF139844

VERSION AF139844.1 GI:4732152
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard, F., Shannon, M., Prak, E.L., Litwin, S. and Weigert, M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard, F. and Weigert, M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr (transgenic/sd-tg)"
/db_xref="taxon:10090"
/chromosome="6"
/clone="50"
/cell_type="B cell hybridoma (spontaneous fusion with
SP2/O)"
/tissue_type="spleen"
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/gene="Igc"
/note="variable region (VJ)"
1..324
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/codon_start=1
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Vk23"
/protein_id="A428631.1"
/db_xref="GI:4732153"
/translation="DIVLTQSPATLSVTPGESVLSCRASQISINLHFWQKSHESHP
RLIKVYASLSISGIPSRFISGSGTDTLINSVETEDFGMYFCQSQDNWPHFTFGST
KLEIKR"
70..105
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/note="CDR1; complementarity determining region 1"
148..168
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265..291
/gene="Igc"
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287..324
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BASE COUNT 88 a 82 c 72 g 82 t
ORIGIN
Query Match 76.1%; Score 244.4; DB 11; Length 324;
Best Local Similarity 85.0%; Pred. No. 1.5e-63;
Matches 272; Conservative 1; Mismatches 47; Indels 0; Gaps 0;
Qy 1 GAGATTGTGCTAAGTCTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
Db 1 GATATTGTGCTAAGTCTCTCCAGCCACCTGTCTGTGACTCCAGGAGAAAGGCTCAGT 60
Qy 61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 120
Db 61 CTTTCTCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCT 120
Qy 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
Db 121 CATGAGTCTCAAGGCTTCTCATCAATATGCTTCCCTGTCATCTCTGGGATCCCGCC 180

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QY 181 AGTTTCAGTGGCAGTGGATCAGGACAGATTTCCACCTCACTATCTCCAGTCTGGAGCCT 240
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QY 241 GAAGATTTTCAGTCTATTACTGTCACACAGTGGCAGTGGCTCAGCAGTTTCGAGAGG 300
Db 241 GAAGATTTTCAGTCTATTACTGTCACACAGTGGCAGTGGCTCAGCAGTTTCGAGATCG 300
QY 301 GGGACCAAGTGGAAATTA 320
Db 301 GGGACCAAGTGGAAATAA 320

RESULT 12
AF139849
LOCUS AF139849 324 bp mRNA ROD 04-NOV-1999
DEFINITION Mus musculus clone 38 immunoglobulin kappa light chain variable
region Vk23 (IgG) mRNA, partial cds.
ACCESSION AF139849
VERSION AF139849.1 GI:4732162
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE 99406777
PUBMED 10477553
REFERENCE 2 (bases 1 to 324)
AUTHORS Brard,F. and Weigert,M.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
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Matches 271; Conservative 2; Mismatches 47; Indels 0; Gaps 0;

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DEFINITION Mus musculus (isolate 3D7.2VK) immunoglobulin light chain (Igl-V)
chain, partial variable region.
ACCESSION L78684
VERSION L78684.1 GI:1374935
KEYWORDS immunoglobulin light chain; variable region.
SOURCE Mus musculus (individual isolate 3D7.2VK, strain MRL-LPR/LPR) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 330)
AUTHORS Gilkeson,G.S., Lefkowitz,J.B. and Di Valerio,R.
TITLE Murine glomerulotrophic monoclonal antibodies are highly
oligoclonal and exhibit distinctive molecular features
JOURNAL J. Immunol. (1996) in press
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Washington Road, Room 401, Princeton, NJ 08544, USA
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ORIGIN

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Best Local Similarity 84.4%; Pred. No. 5e-63; Indels 0; Gaps 0;
Matches 270; Conservative 2; Mismatches 48;
Qy 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGAGAAAGGCGACT 60
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Db 61 CTTTCCTGCCAGGCCAGCAAGATTATAGCAACCACTACACTGGTATCAACAAATCA 120
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Db 121 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTCCAGTCCATCTCTGGGATCCCGTC 180
Qy 181 AGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCACCTCACTCTCCAGTCTGGAGCCT 240
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Qy 301 GGGACCAAGTGGAAATTA 320
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 08:47:13 ; Search time 1450.07 Seconds
(without alignments)
1551.238 Million cell updates/sec

Title: US-08-790-540A-3

Perfect score: 321

Sequence: 1 GAGATTGCTACTCAGTC.....GGACCAAGGTGGAATTAAG 321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	204.4	63.7	398	90	AW405309 UI-HF-BL0
3	201.2	62.7	519	90	AW405183 UI-HF-BL0
4	200.8	62.6	385	90	AW405025 UI-HF-BL0
5	199.6	62.2	468	90	AW405643 UI-HF-BL0
6	199.2	62.1	624	106	BE306691 601104076
7	198	61.7	468	90	AW404506 UI-HF-BL0
8	196.4	61.2	465	90	AW404697 UI-HF-BL0
9	192	59.8	330	90	AW406212 UI-HF-BL0
10	191.6	59.7	514	90	AW405207 UI-HF-BL0
11	191.6	59.7	615	97	AW959456 EST371526
12	191.4	59.6	461	90	AW406219 UI-HF-BL0
13	189.4	59.0	413	90	AW406440 UI-HF-BL0
14	188.4	58.7	409	90	AW406057 UI-HF-BL0
15	186.8	58.2	443	90	AW405460 UI-HF-BL0
16	186.8	58.2	448	90	AW404726 UI-HF-BL0
17	185.6	57.8	708	106	BE309445 601095331
18	185.4	57.8	317	90	AW404261 UI-HF-BL0
19	185	57.6	504	90	AW405787 UI-HF-BL0
20	183.4	57.1	369	90	AW405943 UI-HF-BL0
21	181.8	56.6	518	90	AW406576 UI-HF-BL0
22	181.8	56.6	644	90	AW405817 UI-HF-BL0
23	181.2	56.4	473	90	AW406934 UI-HF-BL0
24	180.4	56.2	425	90	AW406785 UI-HF-BL0
25	180	56.1	604	90	AW405198 UI-HF-BL0
26	179.8	56.0	408	90	AW404674 UI-HF-BL0
27	179.4	55.9	489	90	AW406154 UI-HF-BL0
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34	178.4	55.6	487	89	AW378557 PMO-HT022
35	178.4	55.6	534	92	AW579665 PM2-HT022
36	178.2	55.5	354	90	AW406043 UI-HF-BL0
37	177.6	55.3	355	90	AW405010 UI-HF-BL0
38	177.2	55.2	423	90	AW406796 UI-HF-BL0
39	177	55.1	661	38	AV693657 AV693657
40	177	55.1	686	38	AV698744 AV698744
41	177	55.1	690	38	AV687177 AV687177
42	174.4	54.3	311	90	AW405931 UI-HF-BL0
43	174.2	54.3	412	38	AV695569 AV695569
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ALIGNMENTS

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ACCESSION AW406486
VERSION AW406486.1 GI:6925543
KEYWORDS EST, human.
SOURCE


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VERSION     AW405183.1  GI:6924240
KEYWORDS    EST.
SOURCE      human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 519)
AUTHORS    NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            CDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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RESULT 4
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DEFINITION IMAGE:3058252 5', mRNA sequence.
ACCESSION   AW405025
VERSION     AW405025.1  GI:6924082
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 385)
AUTHORS    NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            CDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
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                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT        88 a 114 c 98 g 85 t
ORIGIN
Query Match      62.6%; Score 200.8; DB 90; Length 385;
Best Local Similarity 76.7%; Pred. No. 2.3e-51;
Matches 244; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

QY 3 GATTGTGCTAATCAGTCTCCAGCCACCTGTCTCTCAGCCCGAGGAGGCGGACTCT 62
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Db 7 GATTGTGTTGACAGTCTCCAGCCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCT 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 TTCTTCGAGCCAGCCAGCAAGTATTAGCACACCCTACACTGTGTATCAACAAGGCGCTGG 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 CTCCTGAGGSCCAGTCTCAGAGTGTTCGAGCTACTTAGCCTGTGTACCAACAAGAACCTGG 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 123 TCAGCCCGCAAGGCTTCTCATCMKKTATGCTTCCAGTCCATCTCTGGGATCCCGGCCAG 182
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QY 183 GTTCAGTGGCAGTGGATCCAGGACAGATTTCCACCTCTACTATCTCCAGTCTGGAGCCTGA 242
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Db 187 GTTCAGTGGCAGTGGGCTCTGGGACAGACTTCACTCTCACCATCAGACCTTAGAGCCTGA 246
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QY 243 AGATTTTGCAGTCTTACTGTCAACAGAGTGGCAGCTGGCCCTCACAGCTTCGGAGGGGG 302
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Db 247 AGATTTTGCAGTCTTACTGTCAACAGAGTGGCAGCTGGCCCTCGGACGTTTCGCCAAGG 306
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QY 303 GACCAAGGTGGAATTA 320
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Db	221	AGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCT	280
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Db	281	GAGATTTTCAGTCTATTTACTGTCAACAGAGTGGCAGCTGGCCTCACAGCTTCGGAGGG	340
QY	301	GGNACCAAGCTGGAAATTA	320
Db	341	GGGACCAAGCTGGAGATCA	360
RESULT 8			
AW0404697	LOCUS	AW0404697	465 bp mRNA EST 16-FEB-2000
DEFINITION	UI-HF-BLJ-acd-b-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058518 5', mRNA sequence.		
ACCESSION	AW0404697		
VERSION	AW0404697.1	GI:6923754	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 465)		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: M13 Forward.		
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BASE COUNT	108 a	139 c	115 g 103 t
ORIGIN			
Query Match 61.2%; Score 196.4; DB 90; Length 465;			
Best Local Similarity 75.8%; Pred. No. 5.5e-50;			
Matches 242; Conservative 1; Mismatches 77; Indels 0; Gaps 0;			
QY	1	GAGATTCAGTCTCACTAGTCTCAGCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGGACT	60
Db	85	GAAATAGATGATGCGGAGTCTCAGCCACCTGTCTGTCTCCAGGGGAAAGGCCACC	144
QY	61	CTTTCGCGCAGGCCAGCCCAAGATTATAGCAACCACTACACTGTATCAACAAGGCCT	120
Db	145	CTCTCTGCGAGGGCCAGTCAGAGTGTATAGCAACAACCTTAGCCCTGGTACCAGCAAAACCT	204
QY	121	GGTCAAGCCCGCAGGGTCTTCATCMKKATATCGTTCAGTCCTCTCTGGATCCCCGCC	180
Db	205	GGCAGGCTCCGAGGTCCTCATCTATGTGGTGCATCCACAGGGCCACTGTGTATCCCGAC	264


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Db 145 CTCCTCTGCAGGCCAGTCAGAGTGTAGCAGCAACTTAGCCTGTGTACAGCAGAGAAATCT 204
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCATCTCTGGGATCCCGGCC 180
Db 205 GCCCAGGCTCCAGGCTCTCATCTATGCTGATCCAGGCGCAGCTGGTATCCAGCC 264
QY 181 AGGTCAGTGGCAGTGATCAGGAGCAGATTTACAGCTCAGCTATCTCCAGTCTGGAGCCT 240
Db 265 AGGTCAGTGGCAGTGGGCTCTGGACAGAGTTCACTCTCACCATCAGCAGCTGCAGTCT 324
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCACACGTTTCGGAGGG 300
Db 325 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGTAAATACTGGCCTCGGACGTTTCGCCCAA 384
QY 301 GGGACCAAGGTGGAATTA 320
Db 385 TGGACCAAGGTGGAATCA 404

RESULT 11
LOCUS AW959456 615 bp mRNA EST 01-JUN-2000
DEFINITION EST371526 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION AW959456
VERSION AW959456.1 GI:8149140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 133
Seq primer: Reverse.
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Best Local Similarity 74.7%; Pred. No. 1.8e-48;
Matches 239; Conservative 1; Mismatches 80; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAAAGGCGACT 60
Db 52 GAAATAGTGATCAGCAGTCTCCAGCCACCTATCTGTCTCCAGGGGAAAGAGCCACC 111
QY 61 CTTTCTGCCAGCCAGCAAGATTTAGCACCACCTACACTGGTATCAACAAGGCT 120
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCATCTCTGGGATCCCGGCC 180
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Db 232 AGGTTCAAGTGGGCTCTGGGACAGAGTACACTTCCACATCAGCAGCTGCAGTCT 291
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGCCTCACACGTTTCGGAGGG 300
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QY 301 GGGACCAAGGTGGAATTA 320
Db 352 GGGACCAAGGTGGAATCA 371

RESULT 12
LOCUS AW406219 461 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BLO-acp-b-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059684 5', mRNA sequence.
ACCESSION AW406219
VERSION AW406219.1 GI:6925276
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 461)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 103 a 136 c 117 g 105 t
ORIGIN
Query Match 59.6%; Score 191.4; DB 90; Length 461;
Best Local Similarity 76.5%; Pred. No. 1.9e-48;
Matches 247; Conservative 1; Mismatches 72; Indels 3; Gaps 1;
QY 1 GAGATTGTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCCGAGAGAAAGGCGACT 60
Db 29 GAATTTGTTGACACAGTCTCCAGCCACCTGTCTTGTCTCCAGGGAAGAGCCACC 88
QY 61 CTTTCTGCCAGGCGCAGCAAGATTTAGCAACACCTACACTGGTATCAACAAGGCT 120
Db 89 CTCCTCTGCAGGCGCAGTCTAGCAGTCTTAGCAGTACTTAGCTGTGTACCAAGAACT 148
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCCACTCTCTGGGATCCCGGCC 180
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Db 149 GGCACGGCTCCAGGCTCCTCAATTAATGATGATCAATCAACAGGGCCACTGGCGTCCAGCC 208
QY 181 AGGTTCAAGTGGAGTGGATCAGGACAGAGATTTTCACTCTCACTATCTCCAGTCTGGAGCCT 240
Db 209 AGGTTCAAGTGGAGTGGGCTGGACAGAGACTTCACTCTCACTACAGAGCCCTAGAGCCT 268
QY 241 GAAGATTTTGCAGTCTATCTACTCTCAACAGAGTGGAGCTGGCCT---CACAGGTTCCGA 297
Db 269 GAAGATTTTGCAGTCTATCTACTCTAGCAGCGTGGAGCTGGCCTCCCTCACTTTCCGGC 328
QY 298 GGGGGACCAAGGTGGAATTA 320
Db 329 GGAGGGACCAAGGTGAGATCAA 351

RESULT 13
LOCUS AW406440 413 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BL0-ach-b-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3060038 5', mRNA sequence.
ACCESSION AW406440
VERSION AW406440.1 GI:6925497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.

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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 92 a 122 c 103 g 96 t
ORIGIN

Query Match 59.0%; Score 189.4; DB 90; Length 413;
Best Local Similarity 77.1%; Pred. No. 7.6e-48;
Matches 229; Conservative 1; Mismatches 67; Indels 0; Gaps 0;

QY 24 AGCCACCTGTCTCTCAGCCAGGAGAGGGGAGTCTTTCTGCGAGGCCAGCAAG 83
Db 8 AGCCACCTGTCTTCTCTCCAGGGAGAGCCACCTCTCTGCGAGGCCAGT 67
QY 84 TATTAGAACCCACTACACTGGTATCAACAAAGCCCTGGTCAAGCCCAAGGCTTCTCAT 143
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QY 144 CMKKTATCGTTCACAGTCCATCTCTGGGATCCCGCCAGGTTCAAGTGGCAGTGCATCAGG 203
Db 128 CTATGATACATCACACGAGCCACTGGCATCCAGCCAGGTTCAAGTGGCAGTGGTCTGG 187
QY 204 GACAGATTTTCAAGTCTACTCTCAGTCTGGAGCCTGAAGATTTTGCAGTCTATCTAGT 263
Db 188 GACAGATTTTCAAGTCTACTCTCAGTCTGGAGCCTAGAGCTTTTGCAGTCTATCTAGT 247
QY 264 TCAACAGAGTGGCAGTGGCCTCACAGTTCGGAGGGGGGACCAAGGTGGAATTA 320
Db 248 TCAGCAGCGTAGCACTGGCCTCTCACTTTCGGGGAGGTCACAGGTGAGATCAA 304

RESULT 14
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IMAGE:3059014 5', mRNA sequence.
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VERSION AW406057.1 GI:6925149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.

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Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 93 a 119 c 107 g 90 t
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Query Match 58.7%; Score 188.4; DB 90; Length 409;
Best Local Similarity 74.1%; Pred. No. 1.5e-47;
Matches 237; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

QY 1 GAGATTTGCTAACTAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGGAGGAGT 60
Db 36 GAAATAGTGAATGATGATGCTCCAGCCACCTGTCTGTCTCCAGGGGAGAGCACC 95
QY 61 CTTTCTGCGAGGCCAGCCAAAGTATTAGCAACCCTACACTGGTATCAACAAAGCCT 120
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QY 121 GGTCAAGCCCCAGGCTTCTCATCMKKTATCGTTCAGTCCATCTCTGGATCCCGCC 180
DB 156 GGGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACTGGTATCCAGCC 215
QY 181 AGGTTCAAGTGGAGTGCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
DB 216 AGGTTCAAGTGGAGTGGGCTCTGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCT 275
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QY 301 GGGACCAAGGTGGAAATTA 320
DB 336 GGGACCAAGGTGGAAATCAA 355

RESULT 15
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DEFINITION UI-HF-BLO-adh-b-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061580 5', mRNA sequence.
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VERSION AW405460.1 GI:6924517
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 443)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.

FEATURES
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 101 a 125 c 116 g 101 t
ORIGIN

Query Match 58.2%; Score 186.8; DB 90; Length 443;
Best Local Similarity 73.8%; Pred. No. 4.9e-47;
Matches 236; Conservative 1; Mismatches 83; Indels 0; Gaps 0;
QY 1 GAGATTGTGCTAAGTCTCAGTCTCCAGCCCGCTCTCTCAGCCGAGAGAGGGCGACT 60
DB 16 GAAGTAGTGTATGACGAGTCTCCAGCCCGCTCTGTGTCTCCAGGGGAGAGCCACC 75
QY 61 CTTTCTCCAGCCGAGCAAGATATTAGCAACCACTACACTGTGTATCAACAAAGGCT 120

DB 76 CTCTCTCGAGGGCGGTGTCAGAGTGTATTAGCAGCAACTTAGCTGTGTCACGAGAGACT 135
QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCATCTCTGGATCCCGCC 180
DB 136 GGGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACTGGTATCCAGCC 195
QY 181 AGGTTCAAGTGGAGTGCAGGACAGATTTACCCCTCACTATCTCCAGTCTGGAGCCT 240
DB 196 AGGTTCAAGTGGAGTGGGCTCTGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCT 255
QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTTCGGAGGG 300
DB 256 GAAGATTTTGCAGTCTATTACTGTGACAGATATAATACTGGCCGCGGCTTCGGCCAA 315
QY 301 GGGACCAAGGTGGAAATTA 320
DB 316 GGGACCAAGGTGGAAATCAA 335

Search completed: February 25, 2001, 08:47:16
Job time: 26051 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:56:38 ; Search time 103.87 Seconds
(without alignments)
1160.949 Million cell updates/sec

Title: US-08-790-540A-3
Perfect score: 321
Sequence: 1 GAGATTGCTACTACAGTC.....GGACCAAGGTGGAAATTAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues
Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	318.6	99.3	321	19 V49821	Vitaxin antibody 1
3	265.8	82.8	321	19 V49823	LM609 antibody lig
4	258.4	80.5	381	21 V35244	Humanised anti-ver
5	250.4	78.0	321	20 V71800	Humanised anti-alp
6	250.4	78.0	338	20 V71802	Vitronectin alpha-
7	245.6	76.5	381	15 O64167	Sequence of mouse
8	239.6	74.6	5238	11 O04654	Plasmid pBT111 enc
9	239.2	74.5	324	20 V71798	Murine vitronectin
10	232.8	72.5	381	21 V35242	Mouse anti-verotox
11	229.6	71.5	416	18 T49345	cDNA encoding kapp
12	228	71.0	324	17 T33446	EGF receptor chime

13	223.6	69.7	486	14	Q43245	hIL2R Ab L chain V
14	223.6	69.7	8858	20	Z10202	Expression vector
15	222	69.2	363	17	T38510	Light chain coding
16	216.6	67.5	315	20	V71803	JK gene segment.
17	216.6	67.5	315	20	V71805	Humanised anti-alp
18	214	66.7	321	20	Z10203	DNA encoding the v
19	213.6	66.5	322	15	Q44714	Light chain variab
20	213.6	66.5	322	20	Z28545	Light chain variab
21	209.2	65.2	321	20	Z10205	DNA encoding the v
22	205.6	64.0	322	14	Q36615	Anti-IL2R-beta ant
23	205.6	64.0	1395	10	N90300	Insert coding for
24	204	63.6	321	14	Q43243	B-B10 Mab L chain
25	204	63.6	321	19	V26766	Anti-gp54 MAB 48-1
26	204	63.6	486	14	Q43384	L-chain V-region o
27	202.8	63.2	642	20	X77408	Anti-human TNF-alp
28	202.4	63.1	381	18	T49338	cDNA encoding kapp
29	202.4	63.1	416	18	T49344	cDNA encoding kapp
30	202.4	63.1	416	18	T49342	cDNA encoding kapp
31	201	62.6	318	14	Q48766	Monoclonal antibod
32	200.8	62.6	381	19	V12262	Monoclonal antibod
33	199.8	62.2	720	19	V26770	Anti-gp54 MAB 48-1
34	199.2	62.1	794	17	T42033	Plasmid pMW152-225
35	199.2	62.1	2070	17	T42035	Plasmid pSW202-225
36	199.2	62.1	2793	17	T42039	Plasmid pMS238-5-2
37	199.2	62.1	2793	17	T42040	Plasmid pMS238-225
38	199.2	62.1	3177	17	T42041	Plasmid pMS240-5-2
39	198.8	61.9	318	19	V54788	DNA encoding the l
40	198.8	61.9	720	19	V54790	scFv comprising he
41	196.4	61.2	720	14	Q40462	Fv(TU27). Homo sa
42	194.4	60.6	717	14	Q40463	Fv(TU25). Homo sa
43	193.8	60.4	429	18	T70811	Mouse anti-idiotyp
44	193.4	60.2	300	13	Q20306	B cell hybridoma 1
45	191.2	59.6	321	18	T87441	Humanised cA2 lig

ALIGNMENTS

RESULT 1	
V49843	ID V49843 standard; DNA; 321 BP.
XX	AC V49843;
XX	DT 02-NOV-1998 (first entry)
DE	LM609 antibody light chain variable region DNA grafted fragment.
XX	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX	macular degeneration; osteoporosis; ss.
OS	Mus sp.
XX	XX
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..321
FT	/*tag- a
FT	/product= "LM609 grafted antibody light chain variable region"
FT	/note= "partial sequence, no start or stop codon given"
XX	WO9833919-A2
XX	06-AUG-1998.
XX	30-JAN-1998; 98WO-US01826.
XX	30-JAN-1997; 97US-0791391.
XX	(IXSY-) IXSYS INC.

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PI Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
DR P-PSDB; W76006.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis.
XX
XX Claim 24; Fig 7; 129pp; English.
XX
XX This sequence encodes a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX and thus block integrin-mediated signal transduction. This is useful in
XX the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
XX
XX
XX Query Match 99.6%; Score 319.8; DB 19; Length 321;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-91;
XX Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
XX Db 1 gagattgtgctaactcagctccagccacctgtctctcagccaggagaagggcgact 60
XX
XX QY 61 CTTTCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCGCT 120
XX Db 61 ctttctgcccagcgccagcaagattagcaaccacctacactggtatcaacaaggcct 120
XX
XX QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGGCC 180
XX Db 121 ggtcaagcccaaggcttctcatcmkktatcggttcagttccatctctgggattccccgcc 180
XX
XX QY 181 AGGTTTCAGTGGCAGTGATGATGATTTTACCCCTCAGTCTCCAGTCTGGAGCGCT 240
XX Db 181 aggttttcagtgagtgatgattgatttttaccctcagttccatctccagttggagcct 240
XX
XX QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGCGAGTGGCCCTCACAGTTCGGAGGG 300
XX Db 241 gaagattttcagctattactgtcaacagatggcagtggtgagtcctcacagttcgagg 300
XX
XX QY 301 GGGACCAAGGTGGAATTAAG 321
XX Db 301 gggaccaaggtggaaattaag 321
XX
XX
XX RESULT 2
XX V49821
XX ID V49821 standard; DNA; 321 BP.
XX AC V49821;
XX
XX 02-NOV-1998 (first entry)
XX
XX Vitaxin antibody light chain variable region DNA.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; ss.
XX
XX Mus sp.

```

```

XX Key Location/Qualifiers
XX CDS 1..321
XX /tag= a
XX /product= "vitaxin antibody light chain variable region"
XX /note= "partial sequence, no start or stop codon given"
XX
XX W09833919-A2.
XX
XX 06-AUG-1998.
XX
XX 30-JAN-1998; 38WO-US01826.
XX
XX 30-JAN-1997; 37US-0791391.
XX (IXSY-) IXSYS INC.
XX
XX Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX P-PSDB; W76002.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX
XX Claim 6; Fig 1b; 129pp; English.
XX
XX This sequence encodes the vitaxin antibody variable light chain region.
XX Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3
XX and can be used to inhibit binding of alphavbeta3 to a ligand and thus
XX block integrin-mediated signal transduction. This is useful in the
XX treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX
XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;
XX
XX
XX Query Match 99.3%; Score 318.6; DB 19; Length 321;
XX Best Local Similarity 99.1%; Pred. No. 4.1e-91;
XX Matches 318; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGCGACT 60
XX Db 1 gagattgtgctaactcagctccagccacctgtctctcagccaggagaagggcgact 60
XX
XX QY 61 CTTTCTGCCAGGCGCAGCAAGTATTAGCAACACCTACACTGTGTATCAACAAGGCGCT 120
XX Db 61 ctttctgcccagcgccagcaagattagcaaccacctacactggtatcaacaaggcct 120
XX
XX QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCAGTCCATCTCTGGGATCCCGGCC 180
XX Db 121 ggtcaagcccaaggcttctcatcmkktatcggttcagttccatctctgggattccccgcc 180
XX
XX QY 181 AGGTTTCAGTGGCAGTGATGATGATTTTACCCCTCAGTCTCCAGTCTGGAGCGCT 240
XX Db 181 aggttttcagtgagtgatgattgatttttaccctcagttccatctccagttggagcct 240
XX
XX QY 241 GAAGATTTCAGTCTATTACTGTCAACAGAGTGCGAGTGGCCCTCACAGTTCGGAGGG 300
XX Db 241 gaagattttcagctattactgtcaacagatggcagtggtgagtcctcacagttcgagg 300
XX
XX QY 301 GGGACCAAGGTGGAATTAAG 321
XX Db 301 gggaccaaggtggaaattaag 321
XX

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RESULT 3
V49823
ID V49823 standard; DNA; 321 BP.
XX
AC V49823;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 antibody light chain variable region DNA fragment.
XX
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT FT /*tag= a
FT FT /product= "LM609 antibody light chain variable region"
FT FT /note= "partial sequence, no start or stop codon given"
XX
PN W09833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
DR WPI; 1998-437472/37.
DR P-PSDB; W75004.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Claim 40; Fig 2b; 129pp; English.
XX
CC This sequence encodes the LM609 antibody variable light chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
XX
SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

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Query Match 82.8%; Score 265.8; DB 19; Length 321;
Best Local Similarity 88.8%; Pred. No. 1.7e-74;
Matches 285; Conservative 2; Mismatches 34; Indels 0; Gaps 0;

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OY 1 GAGATTGCTAATCTCAGTCTCCAGCCACCTGTCTCTCAGCCCGAGGAGAAAGGGGACT 60
   |||||||
DB 1 gatattgtcaactcagctccagccacctgtctgtgacacaggagatagcgtcagt 60
   |||||||
OY 61 CTTTCTCGCCAGCCGACAAAGTATTAGCAACCACTACACTGGTATCAACAAGGCT 120
   |||||||
DB 61 ctttctcgccagccagccagctattagcaaccacctactactggtatcaacaaataca 120
   |||||||

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OY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
   |||||||
DB 121 catgagttctcaaggtcttctcatcagtatcgttcccgatcctctcgtggatccctcc 180
   |||||||
OY 181 AGGTTCAAGTGCAGTGCAGGACAGATTTTCCCTCAGTATCTCCAGTCTGGAGCCT 240
   |||||||
DB 181 aggttcagtgagtcagtcagggacagatttcgtctcagtatcaacagtcgtgagact 240
   |||||||
OY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGCAGTGCCTTCACACGTTCCGAGGG 300
   |||||||
DB 241 gaagattttggaatgtattctgtcaacagatggcagctggccctcacacgttcggagg 300
   |||||||
OY 301 GGGACCAAGTGGAAATTAAG 321
   |||||||
DB 301 gggaccaagctggaaattaag 321
   |||||||

RESULT 4
235244
ID Z35244 standard; cDNA; 381 BP.
XX
AC Z35244;
XX
DT 13-MAR-2000 (first entry).
XX
DE Humanised anti-verotoxin II antibody VTml-1 VL cDNA.
XX
KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;
KW monoclonal antibody; light chain; mouse; human; humanised antibody;
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW HUS; therapy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60 /*tag= a
FT mat_peptide 61..381 /*tag= b
FT FT
FT FT
XX W09959629-A1.
XX PD 25-NOV-1999.
XX PF 19-MAY-1999; 99WO-US11179.
XX PR 20-MAY-1998; 98US-0086570.
XX PA (TEIJ) TEIJIN LTD.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX WPI; 2000-086580/07.
DR P-PSDB; Y32407.
XX
PT Humanized antibody binding to verotoxin II used for treating Verotoxin
PT producing E. coli -
XX
PS Disclosure; Fig 2b; 59pp; English.
XX
CC This DNA sequence codes for a humanised light chain variable region
CC (see Y32407) of murine monoclonal antibody VTml-1 (MuVTml-1), an
CC antibody that specifically binds to the B subunit of verotoxin II
CC (VT2). The invention relates to humanised antibodies against VT2
CC that are capable of neutralizing VT2 and/or VT2 variants. The
CC humanised antibody is a humanized form of MuVTml-1 comprising the
CC complementarity determining regions of MuVTml-1 (see Y32404-05) and
CC heavy and light chain variable region frameworks from the human GF4
CC antibody heavy and light chain frameworks, provided that at least 1
CC position selected from L49, H29, H30, H49 and H98 is occupied by the
CC amino acid at the equivalent position of the MuVTml-1 antibody heavy

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CC or light chain variable region framework. Such humanized antibodies
 CC have an affinity for VT2 that is 3-, 5 or 10-times that of MuVtm1-1.
 CC They are used for treating a patient suffering from, or at risk of,
 CC the toxic effects from VT2 (claimed), especially for treating
 CC verotoxin producing *Escherichia coli* (VTEC) infection, and haemolytic
 CC uraemic syndrome (HUS).
 XX
 SQ Sequence 381 BP; 96 A; 101 C; 85 G; 99 T; 0 other;

Query Match 80.5%; Score 258.4; DB 21; Length 381;
 Best Local Similarity 87.5%; Pred. No. 3.9e-72;
 Matches 280; Conservative 2; Mismatches 38; Indels 0; Gaps 0;
 QY 1 GAGATTGCTCACTCAGCTCCAGCCACCCCTCTCTCTCAGCCCGGAGGAGGCGACT 60
 Db 61 gaaattgtctaactcagctctccagccaccctgtctgtctccaggagaaagagccact 120
 QY 61 CTTTCTGTCGAGCCGACCAAGTATTAGCAACCACTACACTGGTATCAACAAAGGCGCT 120
 Db 121 ctttctcgaggccagtcactattagcaaacactacactggtatcaacaacaaacca 180
 QY 121 GGTCAAGCCCGCAGGCTTCTATCMKKATTCGTTCCCATGCTCCTGGGATCCCGGCC 180
 Db 181 ggtcaggctccaaggcttctcatcaagtctgtctccagtcctatctctggatcccgcc 240
 QY 181 AGGTTCAAGGCGGAGTTCAGGACAGATTTCACCCCTCACTATCTCCAGTCTGGAGCCT 240
 Db 241 aggttcagtgggcagtggaacaggagacagatttcactctcactcagcagctggaatct 300
 QY 241 GAAGATTTCGAGCTATTACTGTCAACAGAGTGGCGCTTCACACGTTTCGGAGGG 300
 Db 301 gaagattttgcagtgattactgtcaacagagattacagtcgctcagctcagttcggtaa 360
 QY 301 GGGACCAAGGTGGAATTA 320
 Db 361 gggaccaagtggaatca 380

RESULT 5
 V71800
 ID V71800 standard; cDNA; 321 BP.
 AC V71800;
 DT 15-MAR-1999 (first entry)
 XX Humanised anti-alpha-v beta-3 MAb D12H2HC 1-0 VL cDNA.
 KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2HC-10; ds.
 XX Homo sapiens.
 OS Synthetic.
 PN W09840488-A1.
 XX 17-SEP-1998.
 XX 12-MAR-1998; 98WO-US04987.
 PR 12-MAR-1997; 97US-0039609.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Johanson KO, Jonak ZL, Taylor AH;
 XX WPI; 1999-034590/03.

DR P-PSDB; W84098.
 XX
 PT New anti alpha-v beta-3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 XX
 PS Claim 2; Page 61-62; 97pp; English.

XX This DNA sequence codes for the light chain variable region (VL,
 CC see W84098) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
 CC (see W84096) of human Kabat subgroup III kappa chain, with
 CC complementarity determining regions from the murine anti-human
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see
 CC W84094). 3 Murine framework residues (1, 49 and 60) are retained
 CC in the synthetic VL. A humanised VH DNA sequence is also provided
 CC (see V71799). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor; e.g. cardiovascular disorders or angio-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.

XX Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 other;

Query Match 78.0%; Score 250.4; DB 20; Length 321;
 Best Local Similarity 85.9%; Pred. No. 1.2e-69;
 Matches 275; Conservative 2; Mismatches 43; Indels 0; Gaps 0;

QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCCGGAGGAGGCGACT 60
 Db 1 gacatagctactgactcagctccagccctgtcttctctccaggagaaagagccacc 60
 QY 61 CTTTCCTGCGAGGCGCAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCGCT 120
 Db 61 ctttctcgaggccagccaaagtattagcaaccactacactggtatcaacaaaaacct 120
 QY 121 GGTCAAGCCCGCAAGGCTTCATCMKKATTCGTTCCAGTCCATCTCTGGGATCCCGGCC 180
 Db 121 ggcacggctcgcggctctctcactcaagtatgcttcccagtcactctctgggataccctcc 180
 QY 181 AGGTTCAAGTGGCAGTGGATCAGGACAGATTTCACCCCTCACTATCTCAGTCTGGAGCT 240
 Db 181 aggttcagtgcaagtgatcagggacagatttcaacttcaccatcagcgcgtctagagcct 240
 QY 241 GAAGATTTCGAGTCTATTACTGTCAACAGAGTGGCAGTGGCTTCACAGTTCGGAGGG 300
 Db 241 gaagattttgcggtttattactgtcaacagagtaacagctggccttttcaogttcggcag 300
 QY 301 GGGACCAAGGTGGAATTA 320
 Db 301 ggtaccaagtggaataaa 320

RESULT 6
 V71802
 ID V71802 standard; cDNA; 338 BP.
 AC V71802;
 DT 15-MAR-1999 (first entry)
 XX Vitronectin alpha-v beta-3 MAB VL cDNA.
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;

Db	67	ctttcttcgagggccgagccaaagtattgacaaacactcactcgtgtatcaacaaaaatca	126
Qy	121	GGTCAAGCCCCAAGGGTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC	180
Db	127	catgagctctccaggctctcattcaataatgcttccagtcctatctctggatccccctct	186
Qy	181	AGGTTCAAGTGGCAGTGTAGCAGGACAGATTTCCACCTCACTATCTCCAGTCTGGGAGCCT	240
Db	187	aggttcagtcgagtgagtcaggagcagatttccactctcagtatcaacagttggagact	246
Qy	241	GAGATTTTCAGTCTATTACTCTCAACAGAGTGGCAGCTGGCGCTCACACGTTTCGGAGGG	300
Db	247	gaagattttggaatgattctctcaccagagacaacagctggcctctcacgcttcctggtct	306
Qy	301	GGGACCAAGGTGGAAATTA 320	
Db	307	gggaccaagctggagctgaa 326	
RESULT	9		
V71798	ID	V71798 standard; cDNA; 324 BP.	
XX	AC	V71798;	
XX	DT	15-MAR-1999 (first entry)	
XX	DE	Murine vitronectin alpha-v beta-3 receptor MAB VL CDNA.	
XX	KW	Humanised antibody; monoclonal antibody; MAB; antibody engineering;	
KW	KW	mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;	
KW	KW	cancer; metastasis; rheumatoid arthritis; atherosclerosis;	
KW	KW	angiogenesis; diabetic retinopathy; inflammation;	
KW	KW	macular degeneration; osteoporosis; Paget's disease;	
KW	KW	hyperparathyroidism; hypercalcaemia; therapy; immunotherapy; ds.	
OS	Mus	sp.	
XX	PN	WO9840488-A1.	
XX	PD	17-SEP-1998.	
XX	PF	12-MAR-1998; '98WO-US04987.	
XX	PR	12-MAR-1997; 97US-0039609.	
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX	PI	Johanson KO, Jonak ZL, Taylor AH;	
XX	PP	WPI; 1999-034590/03.	
DR	DR	P-PSDB; W84094.	
XX	XX	New anti alpha_v beta_3 vitronectin receptor antibodies - used for	
PT	PT	immunotherapeutic treatment of e.g. diabetic retinopathy,	
PT	PT	inflammatory disorders, atherosclerosis, restenosis, cancers or	
PT	PT	osteoporosis	
XX	XX	Example. 13; Page 59-60; 97pp; English.	
XX	XX	This cDNA sequence codes for the light chain variable region (VL,	
CC	CC	see W84094) of the anti-human alpha-v beta-3 vitronectin receptor	
CC	CC	murine monoclonal antibody D12. It was obtained from hybridoma	
CC	CC	total RNA by RT-PCR using mouse kappa and N-terminal-based primers	
CC	CC	(see V71808-09). A heavy chain variable region clone (see V71797)	
CC	CC	has also been identified. D12 VH and VL show sequence similarity	
CC	CC	to Kabat VH subgroup I (see W84095) and Kabat VK subgroup III (see	
CC	CC	W84096), respectively. Humanised VH (see W84097) and VL (see	
CC	CC	W84098) were constructed by combining the framework regions of the	
CC	CC	human v region consensus sequences with complementarity determining	
CC	CC	regions of D12 (keeping some preferred murine framework residues).	
CC	CC	The humanised antibodies are specifically reactive with the human	

CC alpha-v beta-3 protein receptor and capable of neutralising the
CC receptor. They can be used for passive immunotherapy of a disorder
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC disorders or angiogenic-related disorders, such as angiogenesis
CC associated with diabetic retinopathy, atherosclerosis and
CC restenosis, chronic inflammatory disorders, macular degeneration,
CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC diseases where bone resorption is associated with pathology such as
CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
CC of malignancy, osteolytic lesions produced by bone metastasis, bone
CC loss due to immobilisation or sex hormone deficiency. They can also
CC be used for targeted drug therapy, and for detection and diagnosis.
XX
SQ Sequence 324 BP; 85 A; 84 C; 73 G; 82 T; 0 other;

Query Match 74.5%; Score 239.2; DB 20; Length 324;
Best Local Similarity 83.8%; Pred. No. 4e-66; 50; Indels 0; Gaps 0;
Matches 268; Conservative 2; Mismatches 50; Indels 0; Gaps 0;
QY 1 GAGATTGTCTAAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
DB 1 gacattgtgtactcagctccagccaccctgtctgtactccagagatagcgtcagt 60
QY 61 CTTTCTGCCAGCCAGCCCAAGTATTAGCACCCCTACACTGTGTATCAACAAGGCGCT 120
DB 61 cttctctgcaggccagccaaagtattagcaaccactacactggtatcaacaagatca 120
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCTGGATCCCGCC 180
DB 121 catgagctcccaaggtctctcatcagtagtcttccagctcatctctggatccctcc 180
QY 181 AGGTTTCAGTGCAGTGGATCGGACAGATTTACACCTTCTCCAGTCTGGAGCGCT 240
DB 181 aggttcagagcagtgagatcgagcagagattcactctcaatcaatcaaatctggagact 240
QY 241 GAAGATTTGTCAGTCTATTACTGTCAACAGAGTGGCGAGTGCCTCAGCTTCGGAGGG 300
DB 241 gaggttttggagtgattctgtcaacagagataacagctggtcccttcagctcgctcg 300
QY 301 GGGACCAAGGTGGAAATTA 320
DB 301 gggacaacttggaaataaa 320

RESULT 10
235242
ID 235242 standard; CDNA; 381 BP.
XX AC 235242;
XX 13-MAR-2000 (first entry)
DE Mouse anti-verotoxin II antibody VTml-1 VL CDNA.
XX
KW Verotoxin II; VT2; shiga-like toxin; VTml-1; MuvTml-1;
KW monoclonal antibody; light chain; mouse; humanised antibody;
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;
KW HUS; therapy; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /tag= a
FT mat_peptide 58..381
FT /tag= b
FT /transl_except= (pos:184..186, aa:lys)
XX
PN W09959629-A1.
XX
XX 25-NOV-1999.
XX

PF 19-MAY-1999; 99WO-US11179.
PR 20-MAY-1998; 98US-0086570.
XX (TEIJ) TEIJIN LTD.
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX WPI; 2000-086580/07.
DR P-PSDB; Y32405.
XX
PT Humanized antibody binding to verotoxin II used for treating Verotoxin
PT producing E. coli -
XX
PS Disclosure; Fig 1b; 59pp; English.
XX
CC This DNA sequence codes for the light chain variable region (see
CC Y32405) of murine monoclonal antibody VTml-1 (MuvTml-1), an
CC antibody that specifically binds to the B subunit of verotoxin II
CC (VT2). The invention relates to humanised antibodies against VT2
CC that are capable of neutralizing VT2 and/or VT2 variants. The
CC humanised antibody is a humanized form of MuvTml-1 comprising the
CC complementarity determining regions of MuvTml-1 and heavy and
CC light chain variable region frameworks from the human GF4 antibody
CC heavy and light chain frameworks, provided that at least 1 position
CC selected from L49, H29, H30, H49 and H98 is occupied by the amino
CC acid at the equivalent position of the MuvTml-1 antibody heavy or
CC light chain variable region framework. Such humanized antibodies
CC (see Y32406-07) have an affinity for VT2 that is 3-, 5 or 10-times
CC that of MuvTml-1. They are used for treating a patient suffering
CC from, or at risk of, the toxic effects from VT2 (claimed), especially
CC for treating verotoxin producing Escherichia coli (VTEC) infection,
CC and haemolytic uraemic syndrome (HUS).
XX
SQ Sequence 381 BP; 92 A; 98 C; 86 G; 105 T; 0 other;

Query Match 72.5%; Score 232.8; DB 21; Length 381;
Best Local Similarity 82.5%; Pred. No. 4.4e-64;
Matches 264; Conservative 2; Mismatches 54; Indels 0; Gaps 0;
QY 1 GAGATTGTCTAAGTCTCAGCCACCCCTGTCTCTCAGCCAGGAGGAGGCGACT 60
DB 61 gatgtgtgtaactcagctctccagccaccctgtctgtactccagagatagcgtcagt 120
QY 61 CTTTCTGCCAGCCAGCCCAAGTATTAGCACCCCTACACTGTGTATCAACAAGGCGCT 120
DB 121 cttctctgcaggccagctcaactattagcaaacctacactggtatcaacaacataca 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTCCAGTCCATCTCTGGATCCCGCC 180
DB 181 catgagctcccaaggtctctcatcagtagtcttccagctcatctctggatccctcc 240
QY 181 AGGTTTCAGTGCAGTGGATCGGACAGATTTACACCTTCTCCAGTCTGGAGCGCT 240
DB 241 aggttcagtgagcagtgagatcgagcagagattcactctcagtagtcaacagtgtagaaact 300
QY 241 GAAGATTTGTCAGTCTATTACTGTCAACAGAGTGGCGAGTGCCTCAGCTTCGGAGGG 300
DB 301 gaggttttggagtgattctgtcaacagagattacagctggtcccgctcactcttgggtgct 360
QY 301 GGGACCAAGGTGGAAATTA 320
DB 361 gggacccaagctggagactgaa 380
XX
RESULT 11
T49345
ID T49345 standard; CDNA; 416 BP.
XX
AC T49345;
XX

Query Match	71.5%	Score	229.6	DB	18	Length	416
Best Local Similarity	81.9%	Pred. NO.	4.6e-63				
Matches	262	Conservative	2	Mismatches	56	Indels	0
QY	1	GAGATTGGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCCGAGGAGAAAGGGCGACT	60				
Db	76	gaatcgtactgactcagctccagccagcgtgtcttgagtcaggagaaagagccacc	135				
QY	61	CTTTCCTGCCAGGCGCCAAAGTATTAGCAACCACTTACACTGTGTATCAACAAGAGGCT	120				
Db	136	ctctcctcgcagggccagtcagagtatctggcacaacatacacctggtatcagcaagaagacct	195				
QY	121	GGTCAGGCCCCAAGGCTTCTCATCMKKTATCGTTCCCGAGTCGATCTCTGGGATCCCGCC	180				
Db	196	ggccaggctccaaggctctcctataaagtatctcttgatgtctatctctggaaacctcgtgc	255				
QY	181	AGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACCCCTACTCTTCAGTCTGGAGGCT	240				
Db	256	aggtttagtggcagtggaatcagggacagatatttactcttaccatcagcagctgtggagcct	315				
QY	241	GAAGATTGTCAGTCTATTACTGTCTCAACAGAGTGGCAGCTGGCCCTCACACGTTTCGGAGGG	300				
Db	316	gaagattttgcagttta ttactgtcaacaaataataactggccaaacacgctcgtgtgga	375				

	Query Match *	71.08;	Score 228;	DB 17;	Length 324;
	Best Local Similarity	81.6%;	Pred. No. 1.3e-62;		
	Matches 261;	Conservative	Mismatches 57;	Indels	Gaps
QY	1	GAGATTGTGCTAACTCTCTCCAGCCACCCTGTCTCTTCACGCCAGGAGAAAGGGCGACT	60		
	1				
	1				
Db	1	gacatccagctgcgcccsagctccagccacctctctgtgactccagcgagatgcagct	60		
	1				
QY	61	CTTTCTCGCCAGGCGACGCAAGATTAGCAACCACCTTACACTGGTATCAACAAGAGGCT	120		

PI Huse WD, Siadak AW, Thorne BA, Watkins JD, Wu H;
 XX WPI; 1999-527408/44.
 XX Antibody that binds human CD40, for treating T cell mediated
 PT disorders
 XX
 PS Claim 18; Fig 14A-C; 77pp; English.
 XX
 CC The present sequence represents an expression vector for expressing
 CC the light chain of a chimeric anti-CD40 antibody designated ch220.
 CC The antibodies are effective in modulating humoral immune response
 CC against T cell dependent antigens, collagen induced arthritis and
 CC transplant induced rejection. They are also useful for their
 CC anti-inflammatory properties. The antibodies have wide therapeutic
 CC applications, including autoimmune and inflammatory diseases and
 CC transplantation. The antibody can be used in a pharmaceutical composition
 CC for treating a patient suffering from a T cell mediated disorder. They
 CC can also be used to treat autoimmune diseases, inflammatory diseases,
 CC and transplantation.
 XX
 SQ Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;

Query Match 69.7%; Score 223.6; DB 20; Length 8858;
 Best Local Similarity 80.9%; Pred. NO. 1.1e-60;
 Matches 259; Conservative 1; Mismatches 60; Indels 0; Gaps 0;
 QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGGCGGACT 60
 DB 1065 gacattgtctgactcagctccagccaccctgtgtgactccaggagatagctct 1124
 QY 61 CTTTCTCTGCGAGCCAGCCAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCT 120
 DB 1125 cttcttcagggccagccagagattagcagactactactactggtatcaacaaaatca 1184
 QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180
 DB 1185 catgagttcccaaggcttctcacaatgtcttcccatcctcctcctcctcc 1244
 QY 181 AGGTTCACTGGCAGTGGATCAGGGACATTTACCTCCATCTCAGTCTGGAGGCT 240
 DB 1245 aggttcagtgagctgagtgagggctcagattcactcagtcagtcacacagtggtgaa 1304
 QY 241 GAAGATTGTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTGAGGG 300
 DB 1305 gaagatgttggaattattactgtccaacatggtcagagcttccgtggagcttcgggtgga 1364
 QY 301 GGGACCAAGGTGGAAATTAA 320
 DB 1365 ggcaccaagctggaaatcaa 1384

RESULT 15
 T38510
 ID T38510 standard; DNA; 363 BP.
 XX
 AC T38510;
 XX
 DT 23-JUN-1997 (first entry)
 XX
 DE Light chain coding sequence of monoclonal antibody 4B4-1-1.
 KW Antibody; human; heavy chain; variable region; light chain; Mab; 4-1B8;
 KW tumour necrosis factor receptor; membrane protein; accessory molecule;
 KW T-cell; antigen-presenting cell; immune response; rheumatoid arthritis;
 KW immunosuppressive agent; autoimmune disease; rejection response; therapy;
 KW organ transplantation; ss.
 OS Synthetic.
 XX
 XX*
 FH Key Location/Qualifiers
 FT misc_feature 1..324

FT FT /*tag= a
 FT /note= "claimed light chain variable region coding
 FT sequence"
 FT 325..363
 FT /*tag= b
 FT /note= "constant region (encoded protein not given in
 FT specification)"
 XX
 PN WO9632495-A1.
 XX
 PD 17-OCT-1996.
 XX
 PF 06-APR-1996; 36WO-KR00045.
 XX
 PR 08-APR-1995; 35KR-0008176.
 XX
 PA (GLDS) LG CHEM LTD.
 XX
 PI Kang CY, Kim JG;
 XX
 DR WPI; 1996-477143/47.
 DR P-PSDB; W04333.
 XX
 PS Monoclonal antibody specific for human 4-1BB - useful as
 PT immunospecific agent for treating autoimmune diseases and preventing
 PT organ transplant rejection
 XX
 PS Claim 4; Fig 3a; 37pp; English.
 XX
 CC T38509 and T38510 represent the coding sequences for the variable regions
 CC of the heavy and light chains of the antibody of the invention. This
 CC sequence is stated in the specification as being 372 bp in length, but
 CC only comprises 363 bp. The antibody of the invention (designated 4B4-1-1)
 CC is a monoclonal antibody (Mab) specific for human 4-1BB. 4-1BB encodes a
 CC member of the tumour necrosis factor receptor family of integral membrane
 CC proteins. 4-1BB is an accessory molecule expressed on the surface of
 CC T-cells in the initial stage of activation. The accessory molecules on
 CC the T-cell bind to the corresponding ligand on the antigen-presenting
 CC cell and this accelerates the activation of the T- and antigen-presenting
 CC cells, thereby promoting various immune responses. The Mab is specific
 CC for human 4-1BB, which is selectively expressed on activated T-cells. The
 CC Mab is useful as an immunosuppressive agent. It can be used for the
 CC treatment of autoimmune diseases, such as rheumatoid arthritis, and for
 CC preventing rejection response after organ transplantation.
 XX
 SQ Sequence 363 BP; 91 A; 102 C; 79 G; 91 T; 0 other;

Query Match 69.2%; Score 222; DB 17; Length 363;
 Best Local Similarity 80.6%; Pred. NO. 1.1e-60;
 Matches 258; Conservative 1; Mismatches 61; Indels 0; Gaps 0;
 QY 1 GAGATTGTGCTAACTCAGTCTCCAGCCACCCTGTCTCTCAGCCAGGAGGCGGACT 60
 DB 1 gacattgtgagctcagctccagccaccctgtgtgactccaggagatagctct 60
 QY 61 CTTTCTCTGCGAGCCAGCCAGCAAGTATTAGCAACCACTACACTGTGTATCAACAAGGCT 120
 DB 61 cttcttcagggccagccagagattagcagactactactactggtatcaacaaaatca 120
 QY 121 GGTCAAGCCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGATCCCGCC 180
 DB 121 catgagttcccaaggcttctcacaatgtcttcccatcctcctcctcc 180
 QY 181 AGGTTCACTGGCAGTGGATCAGGGACATTTACCTCCATCTCAGTCTGGAGGCT 240
 DB 181 aggttcagtgagctgagtgagggctcagattcactcagtcagtcacacagtggtgaa 240
 QY 241 GAAGATTGTCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACACGTTGAGGG 300
 DB 241 gaagatgttgagtgattactgtccaagatggtcagagcttccgttcagagcttcgggtgga 300
 QY 301 GGGACCAAGGTGGAAATTAA 320

Db 301 ggcaccaagctggaatcaa 320
|| ||||| ||||| ||

Search completed: February 25, 2001, 09:56:42
Job time: 5577 sec

NO WASTE OF TIME

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OM nucleic - nucleic search, using sw model

Run on: February 25, 2001, 09:14:29 ; Search time 75.17 Seconds
(without alignments)
688.206 Million cell updates/sec

Title: US-08-790-540A-3
Perfect score: 321
Sequence: 1 GAGATTGTGCTACTACGTC.....GGACCAAGTGGGAATTAAG 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.6	76.5	381	1	US-07-634-278-82
2	245.6	76.5	381	1	US-08-477-728-82
3	245.6	76.5	381	1	US-08-474-040-82
4	245.6	76.5	381	1	US-08-487-200-82
5	245.6	76.5	424	1	US-08-436-463-3
6	239.6	74.6	5238	5	5453363-1
7	224.8	70.0	321	2	US-08-232-081B-35
8	223.6	69.7	321	2	US-08-232-081B-36
9	222	69.2	324	2	US-08-737-560A-13
10	222	69.2	363	2	US-08-737-560A-8
11	213.6	66.5	322	2	US-08-476-176B-3
12	213.6	66.5	322	3	US-08-127-721A-3
13	213.6	66.5	322	3	US-08-485-246A-3
14	204	63.6	321	2	US-08-232-081B-39
15	201	62.6	318	1	US-08-326-362-3
16	198.8	61.9	318	2	US-08-800-198-3
17	198.8	61.9	318	3	US-09-296-595-3
18	198.8	61.9	720	3	US-08-800-198-7
19	198.8	61.9	720	3	US-09-296-595-7
20	198	61.7	720	2	US-07-956-399-1
21	193.8	60.4	429	2	US-08-653-402B-7
22	191.2	59.6	321	1	US-08-192-102-2
23	191.2	59.6	321	1	US-08-324-799-2
24	191.2	59.6	321	2	US-08-192-861A-2
25	191.2	59.6	717	2	US-07-956-399-3
26	187.2	58.3	812	1	US-08-053-131-178
27	187.2	58.3	812	1	US-08-096-762-178
28	180.8	56.3	900	1	US-08-053-131-180

29 180.8 56.3 900 1 US-08-096-762-180
30 180.4 56.2 931 3 US-09-049-672A-19
31 176.4 55.0 642 2 US-08-480-753-5
32 176.4 55.0 642 3 US-09-041-889-10
33 176.4 55.0 642 3 US-08-837-058-10
34 173.8 54.1 325 4 PCT-US93-12501-1
35 172 53.6 424 2 US-08-476-176B-9
36 172 53.6 424 3 US-08-127-721A-9
37 172 53.6 424 3 US-08-485-246A-9
38 170.8 53.2 321 3 US-08-783-853A-43
39 170.4 53.1 424 2 US-08-476-176B-7
40 170.4 53.1 424 3 US-08-127-721A-7
41 170.4 53.1 424 3 US-08-485-246A-7
42 168.8 52.6 424 2 US-08-476-176B-5
43 168.8 52.6 424 3 US-08-127-721A-5
44 168.8 52.6 424 3 US-08-485-246A-5
45 167.4 52.1 387 2 US-08-480-774A-3

ALIGNMENTS

RESULT 1
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-07-634-278-82

Query Match 76.5% Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGCGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAGCGTCACT 120
QY 61 CTTTCCTGCGAGGAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 121 CTTTCCTGCGAGGAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGTCA 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 240
QY 181 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCTCAAGGCTTCTGGAGCCT 240
DB 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCTCAAGGCTTCTGGAGCCT 300
QY 241 GAAGATTCTGAGTCTTACTGTTCAACAGAGTGCGCCTTCACACGTTGGAGGG 300
DB 301 GAAGATTCTGAGTCTTACTGTTCAACAGAGTGCGCCTTCACACGTTGGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
DB 361 GGGACCAAGTGGAAATTA 380

RESULT 2

US-08-477-728-82
Sequence 82, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
NAME/KEY: CDS
LOCATION: 1..381
US-08-477-728-82

Query Match 76.5% Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAAAGGCGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCTGCTCTCAGCCAGGAGAGCGTCACT 120
QY 61 CTTTCCTGCGAGGAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGGCGCT 120
DB 121 CTTTCCTGCGAGGAGCAAGTATTAGCAACACCTACACTGCTATCAACAAGTCA 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCCATCTCTGGGATCCCGCC 240
QY 181 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCTCAAGGCTTCTGGAGCCT 240
DB 241 AGGTTCAAGTCTCAAGGCTTCTCATCAAGTATGTTCCAGTCTCAAGGCTTCTGGAGCCT 300
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DB 301 GAAGATTCTGAGTCTTACTGTTCAACAGAGTGCGCCTTCACACGTTGGAGGG 360
QY 301 GGGACCAAGTGGAAATTA 320
DB 361 GGGACCAAGTGGAAATTA 380

RESULT 3

US-08-474-040-82
Sequence 82, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COBLENTH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: SCNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-474-040-82

Query Match 76.5%; Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGATAGCGTCACT 120
QY 61 CTTTCTGCGAGCCAGCAAGATTATAGCAACCACTACACTGGTATCAACAAGGCT 120
DB 121 CTTTCTGCGAGCCAGCAAGATTATAGCAACCACTACACTGGTATCAACAAGGCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGTCC 240
QY 241 GAAGATTTGCACTTATTACTGTCAACAGAGTGGGAGTGGGCTCACACGTTCCGAGG 300
DB 301 GAAGATTTGGAATGTATTCTGTCAACAGAGTAAACAGTTGGGCTCATACGTTGGAGGG 360
QY 301 GGGACCAAGCTGGAATTA 320
DB 361 GGGACCAAGCTGGAATTA 380

RESULT 4
US-08-487-200-82
Sequence 82, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung

APPLICANT: SCNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-487-200-82

Query Match 76.5%; Score 245.6; DB 1; Length 381;
Best Local Similarity 85.0%; Pred. No. 5.2e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;

QY 1 GAGATTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGAAAGGGGACT 60
DB 61 GATATTGCTAACTCAGTCTCCAGCCACCCCTGTCTCTCAGCCAGGAGATAGCGTCACT 120
QY 61 CTTTCTGCGAGCCAGCAAGATTATAGCAACCACTACACTGGTATCAACAAGGCT 120
DB 121 CTTTCTGCGAGCCAGCAAGATTATAGCAACCACTACACTGGTATCAACAAGGCT 180
QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCAGTCCATCTCTGGGATCCCGCC 180
DB 181 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCAGTCCATCTCTGGGATCCCGTCC 240
QY 181 AGGTTCAAGTGGGATGAGGACAGATTTCACCCCTCATCTATCTCCAGGCT 240
DB 241 AGGTTCAAGTGGGATGAGGACAGATTTCACCCCTCATCTCTCAAGGCT 300

QY 241 GAAGATTTTGCAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAGACAGTTCGGAGGG 300
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Db 301 GAAGATTTTGGAAATGATTTCTGTCAACAGAGTAACAGTGTGGCTCATACGTTCCGAGGG 360
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QY 301 GGGACCAAGGTGGAATTA 320
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Db 361 GGGACCAAGCTGGAATAAA 380
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RESULT 5
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
US-08-436-463-3
Query Match 76.5%; Score 245.6; DB 1; Length 424;
Best Local Similarity 85.0%; Pred. No. 5.4e-70;
Matches 272; Conservative 2; Mismatches 46; Indels 0; Gaps 0;
QY 1 GAGATTGTCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
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Db 83 GATATTGTCTAACTCAGTCTCCAGCCACCTGTCTGTGACTCCAGGAGATAGCGTCACT 142
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QY 61 CTTTCTGCGCAGCCAGCAAGATTATAGCAACCACTACACTGATGATCAACAAGGGCT 120
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Db 143 CTTTCTGCGCAGCCAGCCAAAGATTATAGCAACCACTACACTGATGATCAACAAGGGCT 202
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
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Db 203 CATGAGTCTCAAGGCTTCTCATCAAGTATGCTTCCCAAGTCCATCTCTGGGATCCCGGCC 262
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QY 181 AGGTTCACTGCAGTGGATCAGGACAGATTCCACCTCAGTATCTCCAGTCTGGAGGCT 240
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Db 263 AGGTTCACTGCAGTGGATCAGGACAGATTTCAGTCTCAGTATCAACAGTGTGGAGACT 322
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QY 241 GAAGATTTTGGAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAGACAGTTCGGAGGG 300
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Db 323 GAAGATTTTGGAAATGATTTCTGTCAACAGAGTAACAGTGGCCTCAGACAGTTCGGTCT 382
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QY 301 GGGACCAAGTGGAAATTA 320
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Db 383 GGGACCAAGCTGGAGCTGAA 402
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RESULT 6
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO: 1:
; LENGTH: 5238
5453363-1
Query Match 74.6%; Score 239.6; DB 5; Length 5238;
Best Local Similarity 84.1%; Pred. No. 1.3e-67;
Matches 269; Conservative 1; Mismatches 50; Indels 0; Gaps 0;
QY 1 GAGATTGTCTAACTCAGTCTCCAGCCACCTGTCTCTCAGCCAGGAGAAAGGGCGACT 60
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Db 7 gatattgtctaactcagtcctccagccacctgtgtgactccaagagatagcgtcagt 66
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QY 61 CTTTCTGCGCAGCCAGCAAGATTATAGCAACCACTACACTGATGATCAACAAGGGCT 120
|||||
Db 67 cttctctgaggccagccaaagtattagcaaacctcacactggtatcaacaaaatca 126
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QY 121 GGTCAAGCCCAAGGCTTCTCATCMKKTATCGTTCCCAAGTCCATCTCTGGGATCCCGGCC 180
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Db 127 catgagtcctcaaggctctctcatcaaatctctccagtcctcctctcggatccccct 186
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QY 181 AGGTTCACTGCAGTGGATCAGGACAGATTTCACCTCAGTATCTCCAGTCTGGAGGCT 240
|||||
Db 187 aggttcagtgagtgagtcagagacagatttcactctcagtatcaacagtgtagact 246
|||||
QY 241 GAAGATTTTGGAGTCTATTACTGTCAACAGAGTGGCAGCTGGCCTCAGACAGTTCGGAGGG 300
|||||
Db 247 gaagattttggaatgtatttctgtcaacagagtaacagctggcctctcacgttcggtgct 306
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QY 301 GGGACCAAGTGGAAATTA 320
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Db 307 gggaccaagctggagctgaa 326
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RESULT 7
US-08-232-081B-35
; Sequence 35, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:

[illegible]

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QY  61  CTTTCTCTGCGCAGGCCAGCCAAAGATTAATAGCAACCACTACACTGCTGATCAACAAGGCTT 120
Db  61  CTTTCTCTGCGCAGGCCAGCCAAAGATTAATAGCAACCACTACACTGCTGATCAACAAGGCTT 120
QY  121  GGTCAGAGCCCCAAGGCTTCTCATCMTKKTATACGTCCGAGTCACATCTCTGGGATCCCGCC 180
Db  121  CATGAGTCTCCAAAGGCTTCTCATCAAAATAGCTTCCCAATTCATCTTGGGATCCCTCC 180
QY  181  AGGTTCAGTGGCAGTGTGATCAGGGACAGATTTACCCCTCATCTCATCTCTGAGGCTT 240
Db  181  AGGTTCAGTGGCAGTGTGATCAGGGACAGATTTACCCCTCATCTCATCTCTGAGGACTT 240
QY  241  GAAGATTTTGCATGCTATTACTGTCAACAGAGTGGCAGCTGGCCCTCACAGCTTGGAGGG 300
Db  241  GAAGATTTTGCAGTGTATTACTGTCAACAGAGTGGTCAAGCTTCCCTCCGAGCTTGGGGA 300
QY  301  GGCACCAAGCTGGAATTA 320
Db  301  GGCACCAAGCTGGAATCAA 320

RESULT 11
US-08-476-176B-3
Sequence 3, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF INVENTION: Immunoglobulin Isotype
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable

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OTHER INFORMATION: domain of murine antibody TES-C21"
US-08-476-176B-3

Query Match          66.5%; Score 213.6; DB 2; Length 322;
Best Local Similarity 78.8%; Pred. No. 9.3e-60;
Matches 252; Conservative 2; Mismatches 66; Indels 0; Gaps

QY 1 GAGATGTGCTAACTACAGTCTCCAGCCACCCCTGTCTCTCAGCCAGAGAAAGGCGACT 60
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Db 1 GACATCTGTGCTAGTCACTGCTCCAGCCATCCTGTCTGTGATCGACAGAGAAAGTCACT 60

QY 61 CTTTCGCCCGGCGACGCCAAGATATAGAACACCACTACAGTGGATATCAACAAAGGCT 120
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QY 121 GGTAAAGCCCAAGCGCTTCATCATCMKRTATCGTCCAGTCCATCTCTGGAGATCCCGCC 180
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Db 121 GATGGTTCTCCAAAGCTTCTCATAAATATGCTTCTGAGTCTATCTCTGGAGATCCCTCC 180

QY 181 AGGTTCACTGACAGTGCATCAGGACAGATTTACACCTCACTATCTCCAGTCTGAGACCT 240
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Db 181 AGGTTATGTCAGTGCATCGATCAGGACAGAGATTTACTATAACATCAACAGTGTGAGTCT 240

QY 241 GAAATTTTGCAGCTCTTACTGTCACACAGAGGCGAGCGGCTCAGTCCAGTTCGAGG 300
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Db 241 GAAATATGTCAGATATTTATCTGTCACAAAGTGAATAGTGGCCAAACAGTTCGAGG 300

QY 301 GGGACCAAGTGGAAATTA 320
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Db 301 GGGACCAAGCTGGAGATAA 320

RESULT 12
US-08-127-721A-3
Sequence 3, Application US/08127721A
Patent No. 6066718
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6066718man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6066718artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA.
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 22-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable"
OTHER INFORMATION: domain of murine antibody TBS-C21"
US-08-127-721A-3

Query Match 66.5%; Score 213.6; DB 3; Length 322;
Best Local Similarity 78.8%; Pred. No. 9.3e-60;
Matches 252; Conservative 2; Mismatches 66; Indels 0; Gaps 0;

QY 1 GAGATGTCCTACTACGCTCCAGCCACCTGCTCTCAGCCGAGGAGAAAGGCGACT 60
DB 1 GACATCTTCTCTAGCTAGCTCCAGCCATCTGCTGTGATGTCAGGAGAAAGTCACT 60
QY 61 CTTTCTGCGCAGGCGCCAGCAAGTATTAGCAACCACTACCTGATATCAAAAGGCT 120
DB 61 TTCTCTGAGGCGCCAGCTAGAGCATGTGCAACAACATACGTGATCAGCAAGAAACA 120
QY 121 GGTCAAGCCCCAGGCTTCTCATCMKKTATCGTTCCCACTCATCTGGAATCCCCGCC 180
DB 121 GATGCTTCTCCAGGCTTCTCATMAAGTATGCTTGTGATCTATCTGTGGATCCCTTC 180
QY 181 AGGTCAGTGGAGTGGATGATCAGGAGATTTACCCCTCATATCCAGTGTGAGGCT 240
DB 181 AGGTTAGTGGAGTGGATGATCAGGAGATTTACTCTTAACATCAGAGTGTGAGTCT 240
QY 241 GAGATTTTGCAGTCTATTAATCTGTCACAGAGTGGCAGCTGCCTCACAGCTTCGAGGG 300
DB 241 GAGATTTTGCAGTCTATTAATCTGTCACAGAGTGGCAGCTGCCTCACAGCTTCGAGGG 300
QY 301 GGGACCAAGGTGGAATTTAA 320
DB 301 GGGACCAAGCTGGAGATTTAA 320

RESULT 13

US-08-485-246A-3
Sequence 3, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against a
TITLE OF INVENTION: Immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6072035artis Patent Department
STREET: 59 Route 10.
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992

ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..321
OTHER INFORMATION: /product= "light chain variable"
OTHER INFORMATION: domain of murine antibody TBS-C21"
US-08-485-246A-3

Query Match 66.5%; Score 213.6; DB 3; Length 322;
Best Local Similarity 78.8%; Pred. No. 9.3e-60;
Matches 252; Conservative 2; Mismatches 66; Indels 0; Gaps 0;

QY 1 GAGATTTGCTACTACGCTCCAGCCACCTGCTCTCAGCCGAGGAGAAAGGCGACT 60
DB 1 GACATCTTCTCTAGCTAGCTCCAGCCATCTGCTGTGATGTCAGGAGAAAGTCACT 60
QY 61 CTTTCTGCGCAGGCGCCAGCAAGTATTAGCAACCACTACCTGATATCAAAAGGCT 120
DB 61 TTCTCTGAGGCGCCAGCTAGAGCATGTGCAACAACATACGTGATCAGCAAGAAACA 120
QY 121 GGTCAAGCCCCAGGCTTCTCATCMKKTATCGTTCCCACTCATCTGGAATCCCCGCC 180
DB 121 GATGCTTCTCCAGGCTTCTCATMAAGTATGCTTGTGATCTATCTGTGGATCCCTTC 180
QY 181 AGGTCAGTGGAGTGGATGATCAGGAGATTTACCCCTCATATCCAGTGTGAGGCT 240
DB 181 AGGTTAGTGGAGTGGATGATCAGGAGATTTACTCTTAACATCAGAGTGTGAGTCT 240
QY 241 GAGATTTTGCAGTCTATTAATCTGTCACAGAGTGGCAGCTGCCTCACAGCTTCGAGGG 300
DB 241 GAGATTTTGCAGTCTATTAATCTGTCACAGAGTGGCAGCTGCCTCACAGCTTCGAGGG 300
QY 301 GGGACCAAGGTGGAATTTAA 320
DB 301 GGGACCAAGCTGGAGATTTAA 320

RESULT 14

US-08-232-081B-39
Sequence 39, Application US/08232081B
Patent No. 5686152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: 150 BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match	63.6%	Score 204	DB 2:	length 321
Best Local Similarity	76.9%	Pred. No.	1, 1e-56	
Matches 246	Conservative	2	Mismatches 72	Indels 0
			Gaps	0

ADDRESS: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

Query Match	62.68%	Score 201	DB 1	Length 318
Best Local Similarity	76.78%	Pred. No.	1e-55	
Matches 243	Conservative	2	Mismatches 72	Indels 0
				Gaps 0

Search completed: February 25, 2001, 09:14:34
Job time: 15049, sec.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:04:13 ; Search time 23.47 Seconds
(without alignments)
309.560 Million cell updates/sec

Title: US-08-790-540a-4

Perfect score: 557

Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHFGGGRVKEIK 107

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_66:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	460	82.6	111	2	S23628
3	458	82.2	128	2	A56701
4	457	82.0	128	2	S40379
5	452.5	81.2	114	2	S54905
6	451	81.0	108	2	G44151
7	447	80.3	106	2	PC4282
8	447	80.3	107	2	B45722
9	444	79.7	117	2	S40362
10	443	79.5	125	2	S40344
11	442	79.4	123	2	S35479
12	441	79.2	107	2	A45722
13	440.5	79.1	109	2	A30608
14	440	79.0	129	2	S29627
15	438	78.6	128	2	S40345
16	437	78.5	107	2	S34005
17	436	78.3	106	2	PL0267
18	433.5	77.8	108	2	B30608
19	433.5	77.8	129	2	A32274
20	432.5	77.6	109	2	G30607
21	431.5	77.5	109	2	K3HUT1
22	431	77.4	107	2	S57444
23	430.5	77.3	109	2	D30601
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25	429.5	77.1	109	2	H30601
26	429	77.0	128	2	S40343
27	428.5	76.9	109	2	K3HUT1
28	427.5	76.8	109	2	G30601
29	427.5	76.8	109	2	B30601

30	427.5	76.8	128	2	S20636	Ig kappa chain V r
31	427.5	76.8	129	1	K3HUT1	Ig kappa chain pre
32	426.5	76.6	215	2	JE0244	Ig kappa chain NIG
33	425.5	76.4	108	2	G30608	Ig kappa chain V-I
34	424.5	76.2	110	2	S20635	Ig kappa chain V r
35	424.5	76.2	129	2	S49532	Ig kappa chain V r
36	423.5	76.0	109	2	PH0963	anti-sm antibody V
37	423.5	76.0	109	2	F30607	Ig kappa chain V r
38	422.5	75.9	109	2	K3HUT1	Ig kappa chain V-I
39	422.5	75.9	129	1	K3HUT1	Ig kappa chain pre
40	420	75.4	114	2	S46375	Ig kappa chain V-J
41	419.5	75.3	130	2	S40360	Ig kappa chain - h
42	419	75.2	138	2	A26471	Ig kappa chain pre
43	417.5	75.0	109	2	F30601	Ig kappa chain V-I
44	417.5	75.0	129	2	S46369	Ig light chain var
45	417.5	75.0	134	2	S38643	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PI0106 Ig kappa chain precursor V-J-C region (LSI) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PI0106

R:Silberstein, L.E., Litvin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PI0106; MUID:89235583

A:Accession: PI0106

A:Molecule type: mRNA

A:Residues: 1-144 <STL>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match 84.4% Score 470; DB 2; Length 144;
Best Local Similarity 85.0% Pred. No. 1.5e-35;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSQASQSIHNLHWYQORPOAPRLTLXYSQSIGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSQASQSVSTLWYQORPOAPRLTLXYSQSIGIPA 80

OY 61 RFSSGSGTDFTLTISLSEPEFAVYICQSGSWPHFGGGRVKEIK 107
DB 81 RFSSGSGTDFTLTISLSEPEFAVYICQSGSWPHFGGGRVKEIK 127

RESULT 2

S23628 Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23628

R:O'Lee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 833-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804

A:Accession: S23628

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>

C:Accession: S35479
R:Takeeda, Y.; Wise, R.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:9237506
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:q197572; PIDD:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F.1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F.13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:28-102/Domain: immunoglobulin homology <IMM>

	Query Match	79.4%	Score 442;	DB 2;	Length 123;
	Best Local Similarity	74.8%*	Pred. No. 4.3e-33;		
	Matches	80;	Conservative	18; Mismatches	9; Indels
					Gaps 0.
Qy	1	EIVLQSPATLSLPERATSLSCQSSQSISNHLHWYQKRGQAPRLIIYYRSQSISGIPA	60		
	:		:::::		
Db	13	DIVLVQSPATLSVTPEDKVLSCSRASQSISNTLHWYQKSHESPRLIITYVSOSISGIPS	72		
Qy	61	RFSGSQGFDTLTLSLEPEDFAVYYYCQSGSMPHTFGGTVEIK	107		
	:		:::::		
Db	73	RFSGSQGFDTLTLSINSVTEDEGAFYCQSSSWMPTFESGITLEIK	119		

RESULT 12
A:55722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (first)
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_Change 21-Jan-2000
C:Accession: A45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez,
J. VIOL. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-90/Domain: Immunoglobulin homology <IM>

Query Match	Similarity	79.2%	Score 441	DB 2	Length 107
Best Local	Similarity 73.8%		Pred. NMC 4.6e-33		
Matches	79	Conservative	18	NonMatches	10
				Indels	0
				Gaps	0

RESULT 13
A30608
Ig kappa chain V-IIJ-region (Son) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C:Accession: A30608
R:Goni, F.R.; Chen, P.P.; McInnis, D.; Arjonailla, M.L.; Fernandez, J.; Carson, D.; Solic
J. Immunol. 142, 3158-3165, 1989

Article: Structural and idiotypic characterization of the L chains of human IGM autocal
A:Reference number: A30601; MUID:89215279
A:Accession: A30608
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-109 <GON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:16-91/Domain: immunoglobulin homology <IIM>

```

Query Match 79.1%; Score 440.5; DB 2; Length 109;
Best Local Similarity 81.5%; Pred. No. 5, 2e-33;
Matches 88; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQAQSGI-SNHLHWYQKPGQAPRLIYRYSQISGIP 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EIVLTQSGTSLTSGEATLSCRAQSVSSYLAHWQKPGQAPRLIYGASNAIQIP 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 60 AAFSSGGSGTDTLTLLISLPEDEFAVYVCOQSGSNPHTFGGATKYEIK 107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NAFSSGGSGTDTLTLLISLPEDEFAVYVCOQYGGSPYFFGGATKYEIK 108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 14
S29627
Ig kappa chain V region (60.3 hybridoma) - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34110; S29627
R:Walls, M.A.; Hsiao, K.; Harris, L.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
A:Reference number: S34110; MUID:93324379
A:Accession: S34110
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <MA2>
A:Cross-references: EMBL:Z17330; NID:g38511; PIDB:CAA76978.1; PID:g38512
A:Note: human sequences cloned and sequenced prior to expression in mouse myeloma ce
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:36-110/Domain: Immunoglobulin homology <IM4>

	Query Match	79.0%	Score 440;	DB 2;	Length 129;
	Best Local Similarity	79.8%;	Pred. 6.7e-33;		
	Matches:	87; Conservative	7; Mismatches	13; Indels	2; Gaps
QY	1 EIVLQSPATISLSGCEATILSCQASQSINHLHMYOORPCQAPRLILXYRSQSISGIPA	60			
DB	21 EIVLQSPATISLSGCEATILSCRASQSVGSILAYLOOKPGQAPRPLLYDASNRTAGIPA	80			
QY	61 RPSGGSGDTFLTITSLLEPEDFAVYYQQQGSSNP--HTFGGTFTVEIK	107			
DB	81 RPSGGSGSDTFTLTITSLLEPEDFAVYYQQHQDNMPGATFGGKIVEIK	129			

S40345
 Ig kappa chain V-J-C region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40345
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; PMID:94080891
 A:Accession: S40345
 A:Status: preliminary; translation not shown

A: Molecule type: mRNA
 A: Residues: 1-128 <KLE>
 A: Cross-references: EMBL:X72455; NID:g441378; PIDN:CA51123.1; PID:g441379
 C: Superfamily: immunoglobulin V region; immunoglobulin homology
 C: Keywords: heterotetramer; immunoglobulin
 F: 32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 438; DB 2; Length 128;
 Best Local Similarity 78.9%; Pred. No. 1e-32;
 Matches 86; Conservative 8; Mismatches 13; Indels 2; Gaps 1;
 QY 1 EIVLTQSPATLSLSPGERATLSCQASQISNHLHWYQQQPGAPRLILYYRSQISGIPA 60
 DB 17 EIVLTQSPATLSLSPGERATLSCRASQSVRIYAWYQQQPGAPRLILYDAINRATGIPA 76
 QY 61 RFGSGSGTDFLTITISLEPEDFAVYCCQSGSMFH--TFGGGTVEIK 107
 DB 77 RFGSGSGTDFLTITISLEPEDFAVYCCQSGSMFPLTFGGGTVEIK 125

Search completed: February 13, 2001, 09:04:14
 Job time: 78 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2001, 09:23:11 ; Search time 14.89 Seconds
(without alignments)
232,066 Million cell updates/sec

Title: US-08-790-540A-4

Perfect score: 357
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHRTGGGTKEIK 107

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	431.5	77.5	109 1	KV3D_HUMAN
2	428.5	76.9	109 1	KV3B_HUMAN
3	427.5	76.8	129 1	KV3L_HUMAN
4	422.5	75.9	109 1	KV3E_HUMAN
5	422.5	75.9	129 1	KV3M_HUMAN
6	418.5	75.1	129 1	KV3H_HUMAN
7	413	74.1	115 1	KV3I_HUMAN
8	410.5	73.7	109 1	KV3F_HUMAN
9	406.5	73.0	108 1	KV3A_HUMAN
10	406	72.9	128 1	KV3K_HUMAN
11	402.5	72.3	109 1	KV3G_HUMAN
12	380	68.2	108 1	KV1H_HUMAN
13	373	67.0	108 1	KV1H_HUMAN
14	371	66.6	111 1	KV3H_MOUSE
15	370	66.4	108 1	KV1J_HUMAN
16	370	66.4	111 1	KV1L_MOUSE
17	370	66.4	111 1	KV3J_MOUSE
18	367.5	66.0	116 1	KV3J_MOUSE
19	367	65.9	129 1	KV1I_HUMAN
20	366	65.7	108 1	KV1E_HUMAN
21	365.5	65.6	100 1	KV3C_HUMAN
22	365	65.5	108 1	KV1V_HUMAN
23	365	65.5	108 1	KV1V_HUMAN
24	365	65.5	115 1	KV5I_MOUSE
25	365	65.5	134 1	KV4C_HUMAN
26	364.5	65.4	133 1	KV4B_HUMAN
27	364	65.4	111 1	KV3J_MOUSE
28	364	65.4	111 1	KV3J_MOUSE
29	364	65.4	114 1	KV4A_HUMAN
30	363	65.2	111 1	KV3U_MOUSE
31	362	65.0	108 1	KV1G_HUMAN
32	361	64.8	111 1	KV3M_MOUSE
33	360	64.6	108 1	KV1N_HUMAN

34	360	64.6	111 1	KV3Q_MOUSE	P01667 mus musculus
35	360	64.6	131 1	KV3I_MOUSE	P01661 mus musculus
36	359	64.5	108 1	KV1K_HUMAN	P01603 homo sapien
37	359	64.5	111 1	KV3S_MOUSE	P01671 mus musculus
38	358	64.3	108 1	KV1B_HUMAN	P01594 homo sapien
39	358	64.3	108 1	KV1R_HUMAN	P01610 homo sapien
40	358	64.3	111 1	KV3D_MOUSE	P03977 mus musculus
41	357.5	64.2	107 1	KV3D_MOUSE	P01596 homo sapien
42	357	64.1	108 1	KV1O_HUMAN	P01611 homo sapien
43	357	64.1	108 1	KV1S_HUMAN	P01607 homo sapien
44	357	64.1	111 1	KV3N_MOUSE	P01666 mus musculus
45	357	64.1	111 1	KV3Q_MOUSE	P01669 mus musculus

ALIGNMENTS

RESULT 1
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622:
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE-72188439; PubMed-5027703;
RA Suter L., Barikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT T1). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HTI.
DR HSSP: P01789; 2MCP.
DR INTERPRO: IPR003006;
DR PFM: PFM0047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CUC749BC CRC64;

Query Match 77.5%; Score 431.5; DB 1; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.8e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

OY 1. EIVLTQSPATLSLSPGERATLSCAQSISN-ELHWYQRPQADRLIYXSQISGIP 59
DB 1 EIVLTQSPATLSLSPGERATLSCRAQSISN-ELHWYQRPQADRLIYXSQISGIP 60
OY 60 ARFSSGGSDFTLTLSLEPEDFAVYCCQSGSWPHRTGGGTKEIK 107
DB 61 DRFSSGGSDFTLTLSLEPEDFAVYCCQSGSWPHRTGGGTKEIK 108

RESULT 2
KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620:
DI 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 RT group."
 RL Biochemistry 20:5816-5822(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01892; K3HUS1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match
 Best Local Similarity 76.9%; Score 428.5; DB 1; Length 109;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQORPGQAPRLLIYRSQISGIP 59
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSYLAWYQORPGQAPRLLIYGASSRATGIP 60
 QY 60 ARSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 107
 DB 61 DRSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 108

RESULT 3
 KY3L_HUMAN STANDARD; PRT; 129 AA.
 ID KY3L_HUMAN
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P10022; K3HUA.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129
 FT DOMAIN 21 43
 FT DOMAIN 44 55
 FT DOMAIN 56 70
 FT DOMAIN 71 77
 FT DOMAIN 78 109
 FT DOMAIN 110 118
 FT DOMAIN 119 129
 FT DISULFID 43 109
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3G5529272774D0 CRC64;

Query Match
 Best Local Similarity 76.8%; Score 427.5; DB 1; Length 129;
 Matches 86; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQORPGQAPRLLIYRSQISGIP 59
 DB 21 EIVLTQSPGTLISLSPGERATLSCRASQSVSYLAWYQORPGQAPRLLIYGASSRATGIP 80
 QY 60 ARSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 107
 DB 81 DRSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 128

RESULT 4
 KY3E_HUMAN STANDARD; PRT; 109 AA.
 ID KY3E_HUMAN
 AC P01623;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046598; PubMed=6794615;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 RT group."
 RL Biochemistry 20:5816-5822(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01896; K3HWT.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 15; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11746 MW; 56C115EBD9CEBE CRC64;

Query Match
 Best Local Similarity 75.9%; Score 422.5; DB 1; Length 109;
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQISN-HLHWYQORPGQAPRLLIYRSQISGIP 59
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSYLAWYQORPGQAPRLLIYGASSRATGIP 60
 QY 60 ARSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 107
 DB 61 DRSSGSGSDFTLTITSSLEPEDFAVYCCQSGSMPTFGGKYEIK 108

RESULT 5
 KY3M_HUMAN STANDARD; PRT; 129 AA.
 ID KY3M_HUMAN
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

RF "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy."
 RL J. Exp. Med. 167:840-852(1988).
 CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR: P10021; K3H0H1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JKI SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 75.9%; Score 422.5; DB 1; Length 129;
 Best Local Similarity 79.6%; Pred. No. 1.9e-37;
 Matches 86; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGAPRLILYXSQISGIP 59
 DB 21 EIVLTQSPATLSLSPGERATLSCQASQSYSSYLAHYQORPGAPRLILYXGASTRATGIPA 80
 QY 60 AEFSSGSGTDFTLTSLSPEDFAVYVYCOQSGSWPHTEGGGKYEIK 107
 DB 81 RFSSGSGTDFTLTSLRLEQEDFAVYVYCOQSGSWPHTEGGGKYEIK 128

RESULT 6

KV3H_HUMAN STANDARD; PRT; 129 AA.

AC P04207;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86177570; PubMed-3083417;
 RA Jirik F.R., Sogge J., Fong S., Heltzmann J.G., Cud J.G., Chen P.P.,
 RA Goldstein R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RT Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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 CC EMBL: M12740; AAA58992.1; -
 DR PIR: A01898; K3H0CL.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 FRAMEWORK 3.
 FT DOMAIN 77 108 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 105 118 FRAMEWORK 3.
 FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 108 JKI SEGMENT.
 FT NON_TER 129 129 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 75.1%; Score 418.5; DB 1; Length 129;
 Best Local Similarity 75.9%; Pred. No. 4.8e-37;
 Matches 82; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSI-SNHLHWYQORPGAPRLILYXSQISGIPA 60
 DB 21 EIVLTQSPATLSLSPGERATLSCQASQSYSSYLAHYQORPGAPRLILYXGASTRATGIPA 80
 QY 61 RFSSGSGTDFTLTSLSPEDFAVYVYCOQSGSW-PHTEGGGKYEIK 107
 DB 81 RFSSGSGTDFTLTSLRLEQEDFAVYVYCOQSGSWPHTEGGGKYEIK 128

RESULT 7

KV3I_HUMAN STANDARD; PRT; 115 AA.

AC P0433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-85087932; PubMed-6440122;
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus."
 RT Nucleic Acids Res. 12:9229-9236(1984).
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 CC EMBL: X01668; -; NOT_ANNOTATED_CDS.
 DR PIR: A01900; K3H0VG.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g: 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 105 118 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 108 JKI SEGMENT.
 FT NON_TER 115 115 BY SIMILARITY.
 SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A1D555 CRC64;

Query Match

74.1%; Score 413; DB 1; Length 115;

Best Local Similarity 83.2%; Pred. No. 1.6e-36;
Matches 79; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 60
DB 21 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 80

QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWP 95
DB 81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWP 115

RESULT 8

KV3F_HUMAN STANDARD; PRT; 109 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE.

RA MEDLINE-76276460; PubMed-60899;
RX Klapper D.G., Capra J.D.;

RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive Igm anti-gamma globulins.";

RL Ann. Immunol. (Paris) 127C:261-271(1976).

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.

CC PIR; A01897; K3HUB6.

DR HSSP; P01789; 2MCP.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 1q; 1.

DR Immunoglobulin V region.

FT DISULFID 23 89

FT NON-TER 109 109

SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 73.7%; Score 410.5; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 2.7e-36;
Matches 81; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 59
DB 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 60

QY 60 ARFSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWPFTGGGTKEIK 107
DB 61 ARFSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWPFTGGGTKEIK 108

RESULT 9

KV3A_HUMAN STANDARD; PRT; 108 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE.

RA Milstein C.;

RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad, F14 and B6.";

FEBS Lett. 2:301-304(1969).

-I-MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.

DR PIR; A01891; K3HUB6.
DR HSSP; P01789; 2MCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1q; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON-TER 108 108
SEQUENCE 108 AA; 11635 MW; 8BC1AF07A419E3D CRC64;

Query Match 73.0%; Score 406.5; DB 1; Length 108;
Best Local Similarity 73.1%; Pred. No. 7.1e-36;
Matches 79; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 59
DB 1 EIVLTQSPATLSLSPGERATLSCAASQSSINHLHWYQORPGQAPRLITLYRSQSIGIPA 60

QY 60 ARFSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWPFTGGGTKEIK 107
DB 61 ARFSGSGTDFTLTISLSEPEDFAVYYCQOQSGSWPFTGGGTKEIK 108

RESULT 10

KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE FROM N.A.

RA MEDLINE-86041852; PubMed-2997711;

RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;

"Human immunoglobulin kappa light chain genes of subgroups II and

III.";

Nucleic Acids Res. 13:6499-6513(1985).

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CC

DR EMBL; 200021; GAA77316.1; -

DR PIR; A01899; K3HUB6.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 1q; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20 IG KAPPA CHAIN V-III REGION IARC/BL41.

FT CHAIN 21 128 FRAMEWORK 1.

FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 44 54 FRAMEWORK 2.

FT DOMAIN 55 69 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 70 76 FRAMEWORK 3.

FT DOMAIN 77 108 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 109 117 FRAMEWORK 4.

FT DOMAIN 118 128 COMPLEMENTARITY-DETERMINING 4.

FT DISULFID 43 108 BY SIMILARITY.

FT NON-TER 128 128

SEQUENCE 128 AA; 14070 MW; CC8957F0EE3B9012 CRC64;

Query Match 72.9%; Score 406; DB 1; Length 128;
Best Local Similarity 74.8%; Pred. No. 9.7e-36;
Matches 80; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

RESULT	12
KYLM_HUMAN	
ID	KYLM_HUMAN
AC	FOI605;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, last sequence update)
DT	15-JUL-1999 (Rel. 38, last annotation update)
DE	IG KAPPA CHAIN V-I REGION LAY.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN	[1]
RP	SEQUENCE.
RA	MEDLINE=77038198; PubMed=824717;
RT	Capra J.D., Klepper D.G.;
RT	"Complete amino acid sequence of the variable domains of two human
RT	IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT	specificities.";
RT	Scand. J. Immunol. 5:677-684(1976).
CC	!!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC	CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN
CC	WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

RESULT	13
KVII_HUMAN	
ID	KVII_HUMAN
STANDARD;	PRT; 108 AA.
AC	P01600;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, last sequence update)
DT	15-JUL-1999 (Rel. 38, last annotation update)
DE	IG KAPPA CHAIN V-I REGION HAV.
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN	[1]
SEQUENCE.	
RP	MEDLINE-71032830; Pubmed-4097974;
RX	"Watanabe S., Hilschmann N.;
RA	"The primary structure of a monoclonal kappa-type immunoglobulin L-
RT	chain of subgroup I (Bence-Jones Protein Hav); subdivision within
RL	subgroups."
CC	Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
DR	P.R. A01868; K1HWHU.
DR	HSSP; P80362; INTL.
DR	INTERPRO: IPR003006; -.
FM	Immunoglobulin V region; Bence-Jones protein.
FT	DOMAIN 1 23 FRAMEWORK 1.
FT	DOMAIN 2 34 FRAMEWORK 2.
FT	DOMAIN 3 56 FRAMEWORK 3.
FT	DOMAIN 4 88 FRAMEWORK 4.
FT	DISULFID 2 23 BY SIMILARITY.
FT	NON_TER 108 108
SEQ	SEQUENCE 108 AA; 11671 MW; 08D3A6160BD8D0618 CRC64;

Query Match	67.0%	Score 373;	DB 1;	Length 108;
Best Local Similarity	65.4%	Pred. No. 2.2e-32;		
Matches 70;	Conservative 20;	Mismatches 17;	Indels 0;	Gaps 0

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; Pubmed=7993911;
RX Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulliez M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RL light chain, dimers.";
RL Biochemistry.33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; Pubmed=6167731;
RX Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human Ki Bence Jones protein wat.";
RJ J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB: 1WTL; 01-NOV-94.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KM Immunoglobulin Y region; Bence-Jones protein; 3d-structure.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 66.4%; Score 370; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 4.6e-32;
Matches 68; Conservative 21; Mismatches 18; Indels 0; Gaps 0.

OY 1 EIVLHNSPATISLISGGERATLSGASQSSISNHLHWYQORPGCAPRLILXYRSQSISGIPA 60
DB 1 DIQMTQSSTLSASVSGDRTYITCRASQDITNYVMFQAPFGCAPKVLIGASILETVGS 60
OY 61 RFGSGSGDTFTLLTISLSEPEDFAVYTCQSGSWPHTEGGGTVEIK 107
DB 61 RFGSGSGDTFTFTTISLSEPEDIAITYCQXYDTLPLTFGGGTGVDIK 107

Search completed: February 13, 2001, 09:23:12
Job time: 1191 sec

```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:04:56 ; Search time 39.42 Seconds

(without alignments)
318.144 Million cell updates/sec

Title: US-08-790-540a-4
Perfect score: 557
Sequence: 1 EIVLTQSPATLSLSPGERAT.....COQSGSWPHTFGGRTVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:***
2: SP bacteria:***
3: SP fungi:***
4: SP human:***
5: SP invertebrate:***
6: SP mammal:***
7: SP mhc:***
8: SP organelle:***
9: SP phage:***
10: SP plant:***
11: SP rodent:***
12: SP virus:***
13: SP vertebrate:***
14: SP unclassified:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429.5	77.1	109	4 Q9UL85	Q9UL85 homo sapien
2	428	76.8	108	4 Q9UL83	Q9UL83 homo sapien
3	427.5	76.8	109	4 Q9UL78	Q9UL78 homo sapien
4	407.5	72.3	109	4 Q9UL86	Q9UL86 homo sapien
5	385	69.1	108	4 Q9UL77	Q9UL77 homo sapien
6	372	66.8	108	4 Q9UL79	Q9UL79 homo sapien
7	366	65.7	108	4 Q9UL70	Q9UL70 homo sapien
8	362.5	65.1	107	4 Q9UL81	Q9UL81 homo sapien
9	338.5	60.8	106	5 Q9UL10	Q9UL10 schistosoma
10	334	60.0	99	11 Q9UL74	Q9UL74 mus musculu
11	334	60.0	107	11 Q9UL84	Q9UL84 mus musculu
12	332	59.6	298	11 Q9UL70	Q9UL70 mus musculu
13	331	59.4	214	11 Q9UL75	Q9UL75 mus musculu
14	326	58.5	101	11 Q9UL78	Q9UL78 mus musculu
15	314	56.4	103	11 Q9UL80	Q9UL80 mus musculu
16	309	55.5	97	11 Q9UL76	Q9UL76 mus musculu
17	309	55.5	114	4 Q9UL80	Q9UL80 mus sapien
18	307.5	55.2	104	11 Q9UL82	Q9UL82 mus musculu
19	280	50.3	109	6 Q9N0W5	Q9N0W5 oryctolagus

20	237	42.5	107	4 Q9UL82	Q9UL82 homo sapien
21	217.5	39.0	107	4 Q9NSD6	Q9NSD6 homo sapien
22	168	30.2	130	4 Q9NP29	Q9NP29 homo sapien
23	150.5	27.0	123	4 Q9UK13	Q9UK13 homo sapien
24	150	26.9	93	4 Q9UL76	Q9UL76 homo sapien
25	146	26.2	123	11 Q61243	Q61243 mus musculu
26	134	24.1	168	4 Q9U056	Q9U056 homo sapien
27	134	24.1	27	4 Q9U055	Q9U055 homo sapien
28	126	22.6	342	13 Q9IRB0	Q9IRB0 spheroides
29	124.5	22.4	331	13 Q9IRB05	Q9IRB05 spheroides
30	123.5	22.2	334	13 Q9IRB05	Q9IRB05 spheroides
31	123.5	22.2	509	11 Q9WTN4	Q9WTN4 mus musculu
32	121.5	21.8	509	11 Q08907	Q08907 mus musculu
33	119	21.4	210	6 P79336	P79336 felis silve
34	118	21.2	152	13 Q9YH11	Q9YH11 ginglymsto
35	117	21.0	100	6 Q77624	Q77624 bos taurus
36	115.5	20.7	119	4 Q9UL84	Q9UL84 homo sapien
37	115.5	20.7	509	11 Q9QX57	Q9QX57 mus musculu
38	115.5	20.7	513	11 P97797	P97797 mus musculu
39	115	20.6	100	13 Q9YH19	Q9YH19 ginglymsto
40	114	20.5	340	13 Q9IRB26	Q9IRB26 spheroides
41	113.5	20.4	333	13 Q9IRB04	Q9IRB04 spheroides
42	113	20.3	136	13 Q9YH19	Q9YH19 ginglymsto
43	113	20.3	136	13 Q9YH16	Q9YH16 ginglymsto
44	112.5	20.2	340	13 Q9IRB20	Q9IRB20 spheroides
45	112	20.1	116	4 Q9UL89	Q9UL89 homo sapien

ALIGNMENTS

RESULT 1
ID Q9UL85 PRELIMINARY; PRT: 109 AA.

AC Q9UL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; RAD56265.1; -;
DR HSP; P01607; IREI.
DR INTERPRO; IPR003006; -;
DR PFAM; PFO0047; 19; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 77.1%; Score 429.5; DB 4; Length 109;
Best Local Similarity 78.7%; Pred. No. 8.8e-41;
Matches 85; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATSCASQSSINHLHWYQRPQADRLILYRSQISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATSCASQSSINHLHWYQRPQADRLILYRSQISGIPA 60
QY 61 RFSGSGGTFTLTLSISLEPEDFAVYYCCQSGSPHT-FPGGRTVEIK 107
DB 61 RFSGSGGTFTLTLSISLEPEDFAVYYCCQSGSPHT-FPGGRTVEIK 108

RESULT 2
ID Q9UL83 PRELIMINARY: PRT: 108 AA.
AC Q9UL83:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -
DR HSSP: P01607; 1RET.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1; 1.
FT NON_TER 1
FT 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA965EA CRC64;

Query Match 76.8%; Score 428; DB 4; Length 108;
Best Local Similarity 76.6%; Pred. No. 1.3e-40;
Matches 82; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 60
DB 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 60
QY 61 RFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 107
DB 61 RFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 107

RESULT 3
ID Q9UL78 PRELIMINARY: PRT: 109 AA.
AC Q9UL78:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1; 1.
FT NON_TER 1
FT 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 76.8%; Score 427.5; DB 4; Length 109;
Best Local Similarity 80.6%; Pred. No. 1.5e-40;

Matches 87; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
QY 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 59
DB 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 60
QY 60 ADFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 107
DB 61 DFFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 108

RESULT 4
ID Q9UL86 PRELIMINARY: PRT: 109 AA.
AC Q9UL86:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1; 1.
FT NON_TER 1
FT 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 72.3%; Score 402.5; DB 4; Length 109;
Best Local Similarity 76.9%; Pred. No. 9.3e-38;
Matches 83; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 59
DB 1 EIVLQSPATLSISPERATLSQASQSI-SNHLHWYQORPGQAPRLIYXSQISGIP 60
QY 60 ADFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 107
DB 61 DFFSGSGSGTDTLTITISLPEDEFAVYVYCOQSGSNPHFTFGGTVEIK 108

RESULT 5
ID Q9UL77 PRELIMINARY: PRT: 108 AA.
AC Q9UL77:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

[illegible]

RESULT 9
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MONOCLONAL ANTI-IDIOCYTIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Strigedidae; Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR HSBP; AF207620; AAF19434.1;
DR HSBP; P01679; 2FBI.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20P544426BAE63E CRC64;

Query Match 60.8%; Score 338.5; DB 5; Length 106;
Best Local Similarity 59.8%; Pred. No. 1.3e-30;
Matches 64; Conservative 18; Mismatches 24; Indels 1; Gaps 1;

QY 1 EIVLTGSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPA 60
DB 1 ENLLTSPALMSASPEKMTMTCSASSVS-YVYWLQKRGSSPRLITDTSLMAGVPV 59
QY 61 RFGSGSGXDTFTLTISLEPEDFAVYVYCOQSGSWPHTFGGKTVK 107
DB 60 RFGSGSGXDTFTLTISLEPEDFAVYVYCOQSGSWPHTFGGKTVK 106
RESULT 10
Q9JL74 PRELIMINARY; PRT; 99 AA.
AC Q9JL74; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206032; AAF69330.1;
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 10939 MW; 3B2D0E78453324 CRC64;

Query Match 60.0%; Score 334; DB 11; Length 99;
Best Local Similarity 61.9%; Pred. No. 3.9e-30;
Matches 60; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 11 LSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPARFSGSGGSTD 70
DB 3 LTVSAGDRTVITCKASQSVSNDAVWYQKPGQSPKLLIYASNRYTGVDRFTSGGYGD 62
QY 71 FTLTISLEPEDFAVYVYCOQSGSWPHTFGGKTVK 107
DB 63 FTFITSTVQEDLAVYFCQODYSPPTEFGGKTVK 99

RESULT 11
Q9JL84 PRELIMINARY; PRT; 107 AA.
AC Q9JL84; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206022; AAF69320.1;
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;

Query Match 60.0%; Score 334; DB 11; Length 107;
Best Local Similarity 58.9%; Pred. No. 4.3e-30;
Matches 63; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 1 EIVLTGSPATLSLSPGERATLSCQASQISNHLHWYQORPGAPRLIYXRSQISGIPA 60
DB 1 DIOMQSTSSLASLDGRXXKXCSASQISNXXMFGQKPDGTVALIYYTSLKSGVS 60
QY 61 RFGSGSGXDTFTLTISLEPEDFAVYVYCOQSGSWPHTFGGKTVK 107
DB 61 RFGSGSGXDTFTLTISLEPEDFAVYVYCOQSGSWPHTFGGKTVK 107

RESULT 12
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CN 8 SCFV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:47 ; Search time 26.34 Seconds
(without alignments)
138.904 Million cell updates/sec

Title: US-08-790-540A-4
Postcode: EE7

Sequence: 1 EIVLTQSPATLSLSPGERAT...CQQSGSWPHTEGGGKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database

- 1: /SDSI/gcgdata/genseq/genseqp/AA1980.DAT: *
- 2: /SDSI/gcgdata/genseq/genseqp/AA1981.DAT: *
- 3: /SDSI/gcgdata/genseq/genseqp/AA1982.DAT: *
- 4: /SDSI/gcgdata/genseq/genseqp/AA1983.DAT: *
- 5: /SDSI/gcgdata/genseq/genseqp/AA1984.DAT: *
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- 7: /SDSI/gcgdata/genseq/genseqp/AA1986.DAT: *
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- 9: /SDSI/gcgdata/genseq/genseqp/AA1988.DAT: *
- 10: /SDSI/gcgdata/genseq/genseqp/AA1989.DAT: *
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- 13: /SDSI/gcgdata/genseq/genseqp/AA1992.DAT: *
- 14: /SDSI/gcgdata/genseq/genseqp/AA1993.DAT: *
- 15: /SDSI/gcgdata/genseq/genseqp/AA1994.DAT: *
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- 18: /SDSI/gcgdata/genseq/genseqp/AA1997.DAT: *
- 19: /SDSI/gcgdata/genseq/genseqp/AA1998.DAT: *
- 20: /SDSI/gcgdata/genseq/genseqp/AA1999.DAT: *
- 21: /SDSI/gcgdata/genseq/genseqp/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	555	99.6	107	19	W76006	LM609 grafted anti
2	555	99.6	107	19	W76002	Vitaxin antibody 1
3	506	90.8	107	13	R25729	Humanised VL region
4	504	90.5	107	20	W84098	Humanised anti-rap
5	504	90.5	112	20	W84100	Vitronectin alpha
6	501	89.9	127	18	W08946	kappa light chain
7	495	88.9	107	18	W08948	kappa light chain
8	495	88.9	107	18	W08949	kappa light chain
9	490	88.0	107	20	Y30205	The variable light
10	489	87.8	107	20	Y30203	The variable light
11	484	86.9	127	21	Y32407	Mouse anti-verotoxin
12	480	86.2	127	15	R50192	Light chain variable

13	480	86.2	127	20	Y26982
14	478	85.8	107	14	R37612
15	474	85.1	107	21	V70604
16	474	85.1	127	15	R50187
17	474	85.1	127	20	Y28980
18	474	85.1	245	21	V70605
19	471	84.6	127	15	R50191
20	471	84.6	127	20	Y26981
21	464	83.3	107	19	W76004
22	450	80.8	105	20	W87456
23	450	80.8	105	20	W87458
24	449.5	80.7	107	18	W24513
25	449	80.6	109	20	Y06380
26	446	80.1	214	20	Y08599
27	440	79.0	349	12	R12128
28	440	79.0	401	12	R12129
29	440	79.0	414	12	R13111
30	440	79.0	414	12	R13018
31	438	78.6	127	15	R54093
32	436.5	78.4	108	21	Y53774
33	436.5	78.4	238	21	Y53775
34	434	77.9	109	15	R55031
35	431	77.4	107	14	R38601
36	431	77.4	107	19	W58482
37	431	77.4	108	12	R15438
38	431	77.4	240	12	R15443
39	430	77.2	111	13	R25721
40	429.5	77.1	104	18	W31723
41	429.5	77.1	107	18	W24514
42	429.5	77.1	110	18	W27545
43	429.5	77.1	129	14	R38672
44	427	76.7	107	14	R38593
45	427	76.7	107	19	W58493

ALIGNMENTS

Result	1	
W76006		
ID	W76006 standard; Protein; 107 AA.	
AC	W76006;	
XX		
DT	02-NOV-1998 (first entry)	
XX		
DE	LM609 grafted antibody light chain variable region protein fragment.	
XX		
VI	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;	
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;	
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy	
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;	
KW	macular degeneration; osteoporosis.	
XX		
OS	Mus. sp.	
XX		
FB	Key	Location/Qualifiers
FT	Misc-difference 49	
FT		/Label- Arg, Met
XX		
PN	W09833919-A2.	
XX		
PD	06-AUG-1998.	
XX		
PF	30-JAN-1998;	98WO-US01826.
XX		
PR	30-JAN-1997;	97US-0791391.
XX		
PA	(IXSY-) IXSYS INC.	
XX		
PI	Glaser SM, Huse WD;	
XX		
DR	WPI; 1998-437472/37.	

DR	N-PSDB; V49843.
XX	
PT	Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT	Integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
P1	angiogenesis or restenosis
XX	
XX	
PS	Claim 19; Fig 7; 129pp; English.
XX	
CC	This sequence represents a LM609 grafted antibody variable light chain
CC	region. LM609 and the antibody vitaxin bind selectively to Integrin
CC	alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a lig
CC	and thus block integrin-mediated signal transduction. This is useful i
CC	the treatment, prevention and diagnosis of alphavbeta3-mediated disease
CC	specifically, angiogenesis and restenosis (but also e.g. (non-)immune
CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC	etc.). The antibodies contain non-murine framework regions so are
CC	suitable for use in humans. Enhanced types of LM609 have affinity more
CC	than 90 times greater than that of parent the parent antibody.
XX	
SO	Sequence 107 AA;

Query Match	99.6%	Score 555	DB 19	length 107
Best Local Similarity	100.0%	Pred. Nc	2.2e-36	
Matches 107; Conservative	0	Mismatches	0	Indels 0; Gaps 0;

[illegible]

QY 61 KFSGSGSGDTFLTILSSLEPEDFAVYICQSSSWPHTEGGGTKEIK 107
 |||||
 61 rfsgsgsgtdftlrisslepedfavyicqsgswphntfggtkveak 107
 Db

RESULT	2
W76002	
ID	W76002 standard; Protein; 107 AA

AC	W76002;
XX	
DT	02-NOV-1998 (first entry)

DE Vitaxin antibody light chain variable region protein fragment

KM Vitreous antibody; variable region; heavy chain; light chain; integrin;
KM LME09; inhibitor; integrin-mediated signal transduction; treatment;
KM diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy
KM neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KM macular degeneration; osteoporosis.

Mus sp

PN WO9833919-A2
XY

PD 06-AUG-1998.
XX

PF 30-JAN-1998; 98MO-0501826.
XX

XX	30-CHAN-1591;	3/6
XX		

XX

XX
DB WPT, 1008-437473/37

DR N-PSDB; V49821.
XX

PT Humanised antibody,
PT integrin - and relat

LMW's, also related nucleic acid, used to treat, prevent or diagnose

PT	angiogenesis or restenosis
XX	
PS	Claim 1; Fig 1b; 129pp; En
..	

CC This sequence represents the vitrxin antibody variable light chain
CC region. Vitrxin and the antibody LM609 bind selectively to integrin
CC α 1b β 3 and can be used to inhibit binding of α 1b β 3 to a
CC ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of α 1b β 3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90-times greater than that of parent the parent antibody.

SQ Sequence 107. AA:

Query Match	99.6%	Score 555	DB 19	Length 107
Best Local Similarity	99.1%	Pred. No.	2.2e-36	
Matches	106	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY 1 EIVLTSPATISLSPGERATISLQASQASISNHLHWYQQRPGAPRLLLXYRSQISGIPA 60
 |||||
 DB 1 EIVLTSPATISLSPGERATISLQASQASISNHLHWYQQRPGAPRLLLKYRSQISGIPA 60

```

QY      61 RFSGSGSGTDFLTLSLEPEDFAVYCCQSGSWPHTFGGGKVEIK 107
      |||
      61 rfsgsgsgtdftltlsslepedfavyccqsgswphftfggtkveik 107
DB

```

RESULT	3
R25729	
ID	R25729 standard; Protein; 107 AA

AC R25729;

DT 13-JAN-1993. (first entry)
XX

Humanised VL region of the mouse CMV5 antibody.

KW gh; light chain; variable region; framework; human; Wol.

Musculus.

FH	Key	Location/Qualifiers
24	24	24

	"CDR"	/note=
FT .	50	56
ET	Position	

FT	Region	/note="CDR"
FT	Region	.89. .97

FT	/note=	"CDR
FT		
FT	Misc-difference:	49

annisset nactetur!!!
-alou/-

XX
FI
XX

173 XX 173

XX 10-DEC-1963 01WQ-TC00711

XX 19-DEC-1990 90MS-0634278
PR

XX. (PROT-²) PROTEIN DESIGN LABS INC.

XX
PI Co MS, Coelling KL, Landolfi NF, Queen CL, Schneider WP;

WPI; 1992-249842/30.

PT New, immunoglobulin(s) having murine CDRs in human framework

CMV, T-cell disorders, myeloid disorders and auto-immune conditions

Claim 40; Fig 27A; 14pp; English.

The sequence shows the humanised mature light chain variable region of the mouse CMV antibody. Murine CDRs were used in a human W01 framework to produce a pure humanised immunoglobulin (Ig) which is capable of binding to the 9H glycoprotein of cytomegalovirus. The Ig is non immunogenic, due to the human framework, and has a strong affinity for its predetermined antigen. They can be produced in large quantities via recombinant DNA and monoclonal antibody technology. The humanised Ig is used alone or in combination with chemotherapeutic agents such as non-steroidal anti-inflammatory drugs or immunosuppressants. See also R25721-32.

Sequence 107 AA;

Query Match 90.8%; Score 506; DB 13; Length 107;
Best Local Similarity 90.7%; Pred. No. 1.3e-32;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATISCSQASQSIISNHLHWYQORPGQAPRLILXYRSQISIGIPA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 elvltqspgtlslspgeratlscraasqslsnhlhwgqkpgqaprlilkyaasqisiglpd 60
OY 61 RSSGSGSDFTLRTISLPEPFAYVYCOQSGSMRPTGGGKXKIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 rfsgsgsldftlrltislepfayvcqsgsmrptfggkxkik 107

RESULT 4

W84098 W84098 standard; Protein: 107 AA.

AC W84098;

DT 15-MAR-1999 (first entry)

DE Humanised anti-alpha-v beta-3 Mab D12HZHC 1-0 VL.

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;

KW macular degeneration; osteoporosis; Paget's disease;

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

KW D12HZHC-10.

OS Homo sapiens.

OS Synthetic.

OS Key

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

Location/Qualifiers
24..34
/label- CDR1
50..56
/label- CDR2
89..97
/label- CDR3

W09840488-A1.

PD 17-SEP-1998.

PF 12-MAR-1998;

PR 12-MAR-1997;

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Johanson KO, Jonak ZL, Taylor AH;

PI

XX WPI: 1999-034590/03.

DR N-PSDB: V71800.

XX #

PT New anti alpha-v beta-3 vitronectin receptor antibodies - used for

PT immunotherapeutic treatment of e.g. diabetic retinopathy,

PT inflammatory disorders, atherosclerosis, restenosis, cancers or

PT osteoporosis

PS Claim 2; Page 61-62; 97pp; English.

This is the amino acid sequence of the light chain variable region (VL) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody D12HZHC 1-0. It is based on the VL sequence (see W84096) of human Kabat subgroup III kappa chain, with complementarity determining regions (CDRs) from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see W84093). 3 Murine framework residues (1, 49 and 60) are retained. The humanised light chain can be expressed in host cells using nucleic acid molecules (see V71800) of the invention. Humanised D12 VH is also provided (see W84097). The humanised antibodies can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or angiogenic-related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.

Sequence 107 AA;

Query Match 90.5%; Score 504; DB 20; Length 107;
Best Local Similarity 89.7%; Pred. No. 1.9e-32;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATISCSQASQSIISNHLHWYQORPGQAPRLILXYRSQISIGIPA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 elvltqspgtlslspgeratlscraasqslsnhlhwgqkpgqaprlilkyaasqisiglpd 60
OY 61 RSSGSGSDFTLRTISLPEPFAYVYCOQSGSMRPTGGGKXKIK 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 rfsgsgsldftlrltislepfayvcqsgsmrptfggkxkik 107

RESULT 5

W84100 W84100 standard; Protein: 112 AA.

AC W84100;

DT 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 Mab VL.

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;

KW macular degeneration; osteoporosis; Paget's disease;

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

OS Mus sp.

OS W09840488-A1.

PD 17-SEP-1998.

PF 12-MAR-1998;

PA 98WO-US04987.

PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;

XX
PD 19-DEC-1996

XX

PF 07-JUN-1996; 96WO-US09847.
XX
XX 15-DEC-1995; 95US-0573289.
PR 07-JUN-1995; 95US-0482982.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (MRC-) MRC COLLABORATIVE CENT.
XX
PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW,
XX
XX WPI: 1997-051897/05.
DR
XX
XX Chimeric and humanised versions of anti-Egf receptor antibody 225 -
PT used for inhibiting tumour growth, esp. of late stage prostatic
PT tumour
XX
XX Claim 29; Fig 21; 112pp; English.
PS
XX The present sequence is the kappa light chain variable region
CC of the reshaped human monoclonal antibody (MAb) H225, 225RKA. The
CC MAb is specific for the human epidermal growth factor (EGF)
CC receptor.
CC The MAb, or a fragment, can be used to inhibit the growth of tumour
CC cells, especially late stage prostatic tumour cells in humans,
CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
CC taxol or cisplatin, or a signal transduction, ras or cell cycle
CC inhibitor.
XX
XX Sequence 107 AA:
SQ

Query Match 88.9%; Score 495; DB 18; Length 107;
Best Local Similarity 87.9%; Pred. No. 9.3e-32;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCAQSOSISNHLHWYQORPGAPRLIXRSQISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCAQSOSISNHLHWYQORPGAPRLIXRSQISGIPA 60

OY 61 RFSGSGSTDFLTITSSLEPEDFAVYVCOQSGSWPHRTGGGTKEIK 107
DB 61 RFSGSGSTDFLTITSSLEPEDFAVYVCOQSGSWPHRTGGGTKEIK 107

RESULT 8
W08949
ID W08949 standard; Protein; 107 AA.
XX
AC W08949;
XX
DT 18-SEP-1997 (first entry)
XX

DE Kappa light chain variable region of 225RB antibody.

XX Kappa; light chain; reshaped; monoclonal; antibody; 225RB;
KW human; epidermal growth factor; EGF; receptor; inhibition; growth;
KW tumour; cell; late stage; prostatic; prostate; variable region;
KW framework; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX

XX Key location/Qualifiers
FH 1..23
FT Region /label- framework_1
FT Region /label- CDR_1
FT Region /label- CDR_1
FT Region /label- framework_2
FT Region /label- CDR_2
FT Region /label- CDR_2
FT Region /label- framework_3
FT Region /label- framework_3
FT Region /label- framework_3

FT /label- CDR_3
FT 98..107
FT Region /label- framework_4
XX
XX W09640210-A1.
XX
XX
XX 19-DEC-1996.
XX
XX
XX 07-JUN-1996; 96WO-US09847.
XX
XX
XX 15-DEC-1995; 95US-0573289.
XX 07-JUN-1995; 95US-0482982.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
PA (MRC-) MRC COLLABORATIVE CENT.
XX
XX Giorgio NA, Goldstein NI, Jones ST, Saldanha JW;
XX
XX WPI: 1997-051897/05.
DR
XX
XX Chimeric and humanised versions of anti-Egf receptor antibody 225 -
PT used for inhibiting tumour growth, esp. of late stage prostatic
PT tumour
XX
XX Claim 29; Fig 21; 112pp; English.
PS
XX The present sequence is the kappa light chain variable region
CC of the reshaped human monoclonal antibody (MAb) H225, 225RKA. The
CC MAb is specific for the human epidermal growth factor (EGF)
CC receptor.
CC The MAb, or a fragment, can be used to inhibit the growth of tumour
CC cells, especially late stage prostatic tumour cells in humans,
CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
CC taxol or cisplatin, or a signal transduction, ras or cell cycle
CC inhibitor.
XX
XX Sequence 107 AA;
SQ

Query Match 88.9%; Score 495; DB 18; Length 107;
Best Local Similarity 87.9%; Pred. No. 9.3e-32;
Matches 94; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSPATLSLSPGERATLSCAQSOSISNHLHWYQORPGAPRLIXRSQISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCAQSOSISNHLHWYQORPGAPRLIXRSQISGIPA 60

OY 61 RFSGSGSTDFLTITSSLEPEDFAVYVCOQSGSWPHRTGGGTKEIK 107
DB 61 RFSGSGSTDFLTITSSLEPEDFAVYVCOQSGSWPHRTGGGTKEIK 107

RESULT 9
Y30205
ID Y30205 standard; Protein; 107 AA.
XX
AC Y30205;
XX
DT 01-NOV-1999 (first entry)
XX

DE The variable light chain of humanised antibody L3.17.

XX Light chain variable region; chimeric antibody; anti-CD40 antibody;
KW chi220; humoral; immune response; T cell dependent antigen;
KW collagen induced arthritis; transplant induced rejection;
KW T cell mediated disorder; autoimmune disease; inflammatory disease;
KW transplantation.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W09942075-A2.
XX

XX PF 19-MAY-1999; 99WO-US11179.
 XX XX 20-MAY-1998; 98US-0086570.
 XX XX (TEIJ) TEIJIN LTD.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX XX Matsunoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
 PI WPI: 2000-086580/07.
 XX DR N-PSDB; 235244.
 DR DR Humanized antibody binding to verotoxin II used for treating Verotoxin
 PT producing E. coli -
 XX XX
 XX PS Claim 12; Fig 2b; 59pp; English.
 XX CC This sequence represents a humanised light chain variable region of
 CC murine monoclonal antibody Vtm1-1 (MuVtm1-1), an antibody that
 CC specifically binds to the B subunit of verotoxin II (VT2). The
 CC invention relates to humanised antibodies against VT2 that are capable
 CC of neutralizing VT2 and/or VT2 variants. The humanised antibody is a
 CC humanized form of MuVtm1-1 comprising the complementarity determining
 CC regions of MuVtm1-1 and the heavy and light chain variable region
 CC frameworks from the human GF4 antibody heavy and light chain
 CC H30, H49 and H98 is occupied by the amino acid at the equivalent
 CC position of the MuVtm1-1 antibody heavy or light chain variable region
 CC framework. Such humanized antibodies have an affinity for VT2 that is
 CC 3-, 5 or 10-times that of MuVtm1-1. They are used for treating a
 CC patient suffering from, or at risk of, the toxic effects from VT2
 CC (claimed), especially for treating verotoxin producing Escherichia
 CC coli (VTEC) infection, and haemolytic uraemic syndrome (HUS).
 XX XX
 XX SO Sequence 127 AA;
 Query Match 86.9%; Score 484; DB 21; Length 127;
 Best Local Similarity 88.8%; Pred. No. 7.6e-31;
 Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EIVLTQSPATISLSPGERATISCOASQSIISNHLHWYQORPGCAPRLIXYSQISIGIPA 60
 DB 21 EIVLTQSPATISLSPGERATISCRASQSIISNHLHWYQKPGQAPRLILKASQISIGIPA 80
 QY 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107
 DB 81 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 127
 RESULT 12
 R50192
 ID R50192 standard; Protein; 127 AA.
 XX AC R50192;
 XX DT 18-OCT-1994 (first entry)
 XX DE Light chain variable region C21-L3 of reshaped antibody.
 XX KW Antibody; heavy chain; light chain; variable region; therapy;
 KW constant region; prophylaxis; prevention; allergy; identification;
 KW allergic reaction; immunoglobulin; IGE; determination.
 XX OS Homo sapiens.
 XX XX
 XX FH Key Location/Qualifiers
 FT Binding-site 44..54
 FT Binding-site /label- CDR 1.
 FT Binding-site 70..76
 FT Binding-site /label- CDR 2.
 FT Binding-site 109..117

FT PF EP589840-A. /label- CDR 3.
 XX XX 30-MAR-1994.
 XX PF 15-SEP-1993; 93EP-0810653.
 XX PR 24-SEP-1992; 92GB-0020228.
 XX PR 25-SEP-1992; 92US-0952802.
 XX PA (CIBA) CIBA GÉIGY AG.
 XX PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Hardman N, Kolbinger F, Saldanha J;
 XX DR WPI: 1994-103410/13.
 DR DR N-PSDB; 044716.
 XX XX
 XX PF New reshaped human monoclonal antibody specific for IGE - used
 PT for prophylaxis or treatment of allergic reactions or qualitative
 PT or quantitative determ. of IGE
 XX XX
 XX PS Example 2; Page 36; 68pp; English.
 XX CC Reshaped human monoclonal antibodies can be used in the prophylaxis
 CC and/or treatment of allergic reactions in humans. The monoclonal
 CC antibodies can also be used for the qualitative or quantitative
 CC determination of IGE and for the determination of surface IGE
 CC positive B cells. They can provide a long lasting therapeutic
 CC effect without inducing immunogenicity as foreign proteins. This
 CC sequence is a slightly modified version of C21-L1 described in
 CC R50187, having glutamic acid at position 1 of the mature protein
 CC instead of aspartic acid and valine at position 3 of the mature
 CC protein instead of leucine (positions 21 and 23 respectively of
 CC this sequence)
 XX XX
 XX SO Sequence 127 AA;
 Query Match 86.2%; Score 480; DB 15; Length 127;
 Best Local Similarity 85.0%; Pred. No. 1.5e-30;
 Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 EIVLTQSPATISLSPGERATISCOASQSIISNHLHWYQORPGCAPRLIXYSQISIGIPA 60
 DB 21 EIVLTQSPATISLSPGERATISCRASQSIISNHLHWYQKPGQAPRLILKASQISIGIPA 80
 QY 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 107
 DB 81 RFSGSGSGTDFTLTITSSLEPEDFAVYYCOQSGSWPHTFGGKVEIK 127
 RESULT 13
 Y26982
 ID Y26982 standard; Protein; 127 AA.
 XX AC Y26982;
 XX DT 24-DEC-1999 (first entry)
 XX DE Light chain variable domain from antibody C21-L3.
 XX KW Diagnosis; IGE; immunoglobulin; body fluid; human; monoclonal antibody;
 KW binding affinity; mouse; CDR; complementarity determining region;
 KW allergy.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN US5958708-A.
 XX PD 28-SEP-1999.

XX 07-JUN-1995; 95US-0476176.
PF 27-SEP-1993; 93US-0127721.
PR 25-SEP-1992; 92US-0932802.
XX (NOV) NOVARTIS CORP.
PA (TANO) TANOX BIOSYSTEMS INC.
XX
PI Saldanha J, Kolbinger F, Hardman N;
XX WPI: 1999-570765/48.
DR N-PSDB: 228548.
XX
PI new method for determining IGE levels in a sample
XX
PS Disclosure: Column 41-42; 19pp; English.
XX The invention relates to a method of determining IGE levels in a body
CC fluid sample, by contacting the sample with a reshaped human monoclonal
CC antibody (RA) having a binding affinity about equal to that of the
CC murine CDR-donor antibody TES-C21 produced by the cell line 11133.
CC The antibodies are useful in the diagnosis, prophylaxis and treatment
CC of allergy. This sequence represents the light chain variable domain
CC from the reshaped human antibody C21-L3.
XX
SQ Sequence 127 AA;

Query Match 86.2%; Score 480; DB 20; Length 127;
Best Local Similarity 85.0%; Pred. No. 1.5e-30;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 EIVLQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGAPRLILYXSQISGIPA 60
DB 21 elvltqspatlsispgeratlsqcrasqstgltlnhwyqgqrpqaprlilkyasesisgip 80
QY 61 RFGSGSGTDFTLTISLSEPEDFAVYICQSGSWPHTFGGTRVEIK 107
DB 81 rfsqsgsgtdftltisrlepedfavyicqsgswphtfggtrkveik 127

RESULT 14
R37612 standard; Protein; 107 AA.
ID R37612;
AC R37612;
XX 13-OCT-1993 (first entry)
DT
XX
DE hIL2R Ab L chain V region.
XX
KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
KW human; Interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
KW region; PCR; framework; plasmid; heavy; H; light; L.
XX
OS Mus musculus/Homo sapiens.
XX
FN WO9311238-A.
XX
PD 10-JUN-1993.
XX
PF 03-DEC-1992; 92MO-JP01583.
XX
PR 06-DEC-1991; 91JP-0323319.
XX
XX (BIOT) BIOTEST PHARMA GMBH.
PA (INNO) INNOTHERAPIE LAB.
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Gomi H, Nakatani T, Noguchi H, Wajdenes J;
XX

DR WPI: 1993-197057/24.
DR N-PSDB: Q43245.
XX
XX Humanised antibody comprising - CDR region of mouse MAB B-B10
PI specific for IL-2 receptor useful for treating carcinoma
PT expressing IL-2 receptor
XX
PS Claim 2; Fig 5; 62pp; English.
XX
XX The sequences given in R37611-12 represent the heavy (H) and light (L)
CC chain variable (V) regions of a humanised antibody (Ab) which binds
CC specifically to human Interleukin (IL)-2 receptor (hIL2R). The
CC complementarity-determining regions (CDRs) of these V regions were
CC derived from the murine anti-human IL-2 receptor monoclonal Ab (Mab)
CC B-B10 (see also R37599-04). This Mab is antagonistic to the binding
CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
CC the human mixed lymphocyte reaction. The cDNA encoding the variable
CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
CC sequence homology to the murine sequence was selected and the
CC framework of this Ab was bound with the B-B10 V region CDR and a
CC part of the framework to design several kinds of the humanised B-B10
CC V region. The DNA sequence coding this humanised B-B10 was
CC synthesised and a plasmid expressing humanised B-B10 was constructed.
XX
SQ Sequence 107 AA;

Query Match 85.8%; Score 478; DB 14; Length 107;
Best Local Similarity 86.0%; Pred. No. 1.9e-30;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 EIVLQSPATLSLSPGERATLSCQASQSIHNLHWYQORPGAPRLILYXSQISGIPA 60
DB 1 elvltqspatlsispgeratlsqcrasqstgltlnhwyqgqrpqaprlilkyasesisgip 60
QY 61 RFGSGSGTDFTLTISLSEPEDFAVYICQSGSWPHTFGGTRVEIK 107
DB 61 rfsqsgsgtdftltisrlepedfavyicqsgswphtfggtrkveik 107

RESULT 15
Y70604 standard; Protein; 107 AA.
ID Y70604;
AC Y70604;
XX 18-JUL-2000 (first entry)
DT
XX
DE V kappa region of humanised antibody Hu-901.
XX
KW Humanised antibody-901; Hu-901; V kappa; kappa chain variable region;
KW anti-IGE; anti-immunoglobulin E; monoclonal antibody; hybridoma TES-C21;
KW recombinant adenovirus vector; anti-IGE antibody; gene therapy; scfv;
KW single chain variable fragment; allergy; anti-allergic.
XX
OS Homo sapiens.
XX
FN WO200015260-A1.
XX
PD 23-MAR-2000.
XX
PF 16-SEP-1999; 99WO-US21646.
XX
PR 16-SEP-1998; 98US-0100639.
XX
XX (TANO) TANOX INC.
PA
PI Liou RS, Thomas D;
XX
DR WPI: 2000-271264/23.
DR N-PSDB: 252078.

XX New nucleic acids encoding anti-IgE antibodies such as Hu-901 or their
 PT fragments, useful in the gene therapy of allergic diseases -
 XX
 PS Disclosure; Page 47; 52pp; English.

CC The present protein sequence is the Ykappa (kappa chain variable region)
 CC of the humanised antibody Hu-901. This is an exemplary anti-IgE (anti-
 CC -immunoglobulin E) monoclonal antibody produced by hybridoma TES-C21. The
 CC heavy and light chains are obtained through RT-PCR using the RNA from the
 CC transfectoma cell line producing the chimeric antibody. Humanised
 CC anti-IgE genes are incorporated in the genome of a recombinant adenovirus
 CC vector as an independent transcriptional unit, and packaged into
 CC infectious virus particles. Upon infection of host, the recombinant
 CC adenovirus vector will direct the production of either intact anti-IgE
 CC antibody or an scFv fragment in the serum, which will bind free
 CC circulating IgE, resulting in the reduction of free serum IgE. The
 CC binding of the antibody or fragment to IgE-bearing B cells may lower IgE
 CC levels by down-regulating IgE production by these B cells. These methods
 CC are useful in the gene therapy of allergic diseases.

XX
 SQ Sequence 107 AA;

Query Match 85.1%; Score 474; DB 21; Length 107;
 Best Local Similarity 83.2%; Pred. No. 3.8e-30;
 Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVLTSPATLSLSPERATLSQASQSTSNHLHWYQORPGAPRLILYRSOSISGIPA 60
 DB 1 dilltspgtlslsperatlscraasgslgtnhwgkpgqgprlllkysaslsiglds 60
 QY 61 RFGSGSGTDFITITISLEPEDFAVYVCOOSGSMPTFGGTFVEIK 107
 DB 61 rfsqsgsgtdftltlsrlepedfamyvqgsdswptlfgqgkveik 107

Search completed: February 13, 2001, 09:03:48
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OM protein - protein search, using sw model

Run on: February 13, 2001, 09:03:16 ; Search time 18.5 Seconds

(without alignments)
103.860 Million cell updates/sec

Title: US-08-790-540A-4

Perfect score: 557

Sequence: 1 EIVLTQSPARLSLSPGERAT.....COQSGSWPHTFGGKTVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	90.8	107	US-07-634-278-63	Sequence 63, Appl
2	506	90.8	107	US-07-634-278-87	Sequence 87, Appl
3	506	90.8	107	US-08-477-728-63	Sequence 63, Appl
4	506	90.8	107	US-08-477-728-87	Sequence 87, Appl
5	506	90.8	107	US-08-474-040-63	Sequence 63, Appl
6	506	90.8	107	US-08-474-040-87	Sequence 87, Appl
7	506	90.8	107	US-08-487-200-63	Sequence 63, Appl
8	506	90.8	107	US-08-487-200-87	Sequence 87, Appl
9	480	86.2	127	US-08-476-176B-10	Sequence 10, Appl
10	480	86.2	127	US-08-485-246A-10	Sequence 10, Appl
11	480	86.2	127	US-08-476-176B-6	Sequence 6, Appl
12	474	85.1	127	US-08-127-721A-6	Sequence 6, Appl
13	474	85.1	127	US-08-485-246A-6	Sequence 6, Appl
14	474	85.1	127	US-08-485-246A-9	Sequence 9, Appl
15	473	84.9	127	US-08-476-176B-8	Sequence 8, Appl
16	471	84.6	127	US-08-127-721A-8	Sequence 8, Appl
17	471	84.6	127	US-08-485-246A-8	Sequence 8, Appl
18	471	84.6	127	US-08-783-853A-44	Sequence 44, Appl
19	449.5	80.7	107	US-07-634-278-62	Sequence 62, Appl
20	441	79.2	107	US-08-477-728-62	Sequence 62, Appl
21	441	79.2	107	US-08-474-040-62	Sequence 62, Appl
22	441	79.2	107	US-08-487-200-62	Sequence 62, Appl
23	441	79.2	127	US-07-634-278-83	Sequence 83, Appl
24	441	79.2	127	US-08-477-728-83	Sequence 83, Appl
25	441	79.2	127	US-08-474-040-83	Sequence 83, Appl
26	441	79.2	127	US-08-487-200-83	Sequence 83, Appl
27	441	79.2	127	US-08-436-463-4	Sequence 4, Appl
28	438	78.6	127	US-08-436-463-4	Sequence 4, Appl

29	434	77.9	107	US-08-436-463-20	Sequence 20, Appl
30	434	77.9	109	US-07-942-245-4	Sequence 4, Appl
31	432.5	77.6	107	US-08-783-853A-57	Sequence 57, Appl
32	431	77.4	107	US-08-107-669D-1	Sequence 1, Appl
33	431	77.4	107	US-08-477-788A-1	Sequence 1, Appl
34	431	77.4	107	US-08-477-531B-1	Sequence 1, Appl
35	431	77.4	107	US-08-082-842A-1	Sequence 1, Appl
36	430.5	77.3	108	US-08-232-081B-42	Sequence 42, Appl
37	430	77.2	111	US-07-634-278-47	Sequence 47, Appl
38	430	77.2	111	US-08-477-728-47	Sequence 47, Appl
39	430	77.2	111	US-08-474-040-47	Sequence 47, Appl
40	430	77.2	111	US-08-487-200-47	Sequence 47, Appl
41	429.5	77.1	107	US-08-783-853A-62	Sequence 62, Appl
42	427	76.7	107	US-08-107-669D-14	Sequence 14, Appl
43	427	76.7	107	US-08-477-788A-14	Sequence 14, Appl
44	427	76.7	107	US-08-477-531B-14	Sequence 14, Appl
45	427	76.7	107	US-08-082-842A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-63
Sequence 63, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: ODEEN, Gary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLF, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-634-278-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPA 60
Db 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPD 60

QY 61 RFSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
Db 61 RFSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107

RESULT 2

US-07-634-278-87
Sequence 87, Application US/07634278
Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634, 278
CLASSIFICATION: 424
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590, 274
FILING DATE: 28-SEP-1990

APPLICATION DATA:
APPLICATION NUMBER: US 07/310, 252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290, 975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-87

Query Match 90.8%; Score 506; DB 1; Length 107;

Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPA 60
Db 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPD 60

QY 61 RFSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107
Db 61 RFSGSGSGTDFLTLLISLPEDEFAVYCCQSGSWPHTFGGTRVEIK 107

RESULT 3

US-08-477-728-63
Sequence 63, Application US/08477728
Patent No. 5585089

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634, 278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590, 274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310, 252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290, 975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPA 60
Db 1 EIVLTOSPTATLSLSPGERATLSCQASQSSISNHLHWYQORPGAPRLIXRSQISGIPD 60

Db 1 EIVLTQSPGTLISLSPGERATLISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
Db 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

RESULT 4

US-08-477-728-87
Sequence 87, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATISLSPGERATISCSASQISNNLHWYQQKPGAPRLILIKYASQISIGIPA 60
Db 1 EIVLTQSPGTSLSPGERATISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
Db 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

US-08-474-040-63
Sequence 63, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATISLSPGERATISCSASQISNNLHWYQQKPGAPRLILIKYASQISIGIPA 60
Db 1 EIVLTQSPGTSLSPGERATISCRASQISNNLHWYQQKPGAPRLILIKYASQISIGIPD 60
QY 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107
Db 61 RSSGSGGTDFLTITISLSEPEDFAVYYCOQSGSWPHTFGGKTKVEIK 107

RESULT 6

US-08-474-040-87
; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-87

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIISNHLHWYQQRPGAPRLILXYSSQISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIISNHLHWYQQRPGAPRLILXYSSQISGIPD 60
QY 61 RSSGSGSTDTLTITSLSEPEDFAVYYCOQSGSNPHTFGGKVEIK 107
DB 61 RSSGSGSTDTLTITSLSEPEDFAVYYCOQSGSNPHTFGGKVEIK 107

RESULT 7
US-08-487-200-63
; Sequence 63, Application US/08487200
; Patent No. 5693762
; APPLICANT: QUEEN, Cary L.

GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-487-200-63

Query Match 90.8%; Score 506; DB 1; Length 107;
Best Local Similarity 90.7%; Pred. No. 9.1e-41;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCQASQSIISNHLHWYQQRPGAPRLILXYSSQISGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCQASQSIISNHLHWYQQRPGAPRLILXYSSQISGIPD 60
QY 61 RSSGSGSTDTLTITSLSEPEDFAVYYCOQSGSNPHTFGGKVEIK 107
DB 61 RSSGSGSTDTLTITSLSEPEDFAVYYCOQSGSNPHTFGGKVEIK 107

RESULT 8
US-08-487-200-87
; Sequence 87, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.

RESULT 9
US-08-476-176B-10
: Sequence 10, Application US/08476176B
: Patent No. 5958708
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 5958708man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saldanña, Jose

```

Query Match      86.2%  Score 480;  DB 2;  Length 127;
Best Local Similarity 85.0%  Pred. No. 2.9e-38;
Matches 91;  Conservative 7;  Mismatches 9;  Indels 0;  Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCAASGSIINHLAHYQORPCQAPRLILYRDSISIGIPA 60
    |||||.....:|||||:|||||:|||||:|||||:
Db 21 EIVLTQSGTISLSPGERATLSCRASGSIIGINIHYYQKPCQAPRLILIKYSESISIGIPS 80
    |||||.....:|||||:|||||:|||||:|||||:

QY 61 RFSSGSGSTDTFTLTITSLSPEDFAVYYCOQSGSWPHRTGGGCTKVEIK 107
    |||||.....:|||||:|||||:|||||:|||||:
Db 81 RFSSGSGSTDTFTLTITSLRLEPEDFAMYYCOQSDSWPTTGGGCTKVEIK 127
    |||||.....:|||||:|||||:|||||:|||||:

```

ADDRESS: No. 6066718attls Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-127-721A-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 2.9e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVTQSPATLSLSPGERATLSCQASQSI SNHLHWYQORPGQAPRLIXYSQISIGIPA 60
DB 21 EIVTQSPATLSLSPGERATLSCQASQSI GTNINHWYQORPGQAPRLIXYASISIGIPS 80
QY 61 RSSGSGSGDTFTLTSSLEPEDFANYCCQSGSWPHTFGGKVEIK 107
DB 81 RSSGSGSGDTFTLTSSLEPEDFANYCCQSGSWPHTFGGKVEIK 127

RESULT 11
US-08-485-246A-10
Sequence 10, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 6072035artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.

REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-10

Query Match 86.2%; Score 480; DB 3; Length 127;
Best Local Similarity 85.0%; Pred. No. 2.9e-38;
Matches 91; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIVTQSPATLSLSPGERATLSCQASQSI SNHLHWYQORPGQAPRLIXYSQISIGIPA 60
DB 21 EIVTQSPATLSLSPGERATLSCQASQSI GTNINHWYQORPGQAPRLIXYASISIGIPS 80
QY 61 RSSGSGSGDTFTLTSSLEPEDFANYCCQSGSWPHTFGGKVEIK 107
DB 81 RSSGSGSGDTFTLTSSLEPEDFANYCCQSGSWPHTFGGKVEIK 127

RESULT 12
US-08-476-176B-6
Sequence 6, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
APPLICANT: Hardman, No. 5958708man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-6

APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA

COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,081B
 FILING DATE:

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
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 REFERENCE/DOCKET NUMBER: 20-3484
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 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-232-081B-9

Query Match 84.9%; Score 473; DB: 2; Length 107;
 Best Local Similarity 85.8%; Pred No. 1.1e-37;
 Matches 91; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY	1	EIVLTQSPATLSLSPGERATLSCQASQSTISNHLHWYQQRPGQAPRLILYRSQSIGIPA	60
DB	1	EIVLTQSPATLSLSPGERATLSCRASQITGTSIHWYQQRPGQAPRLILYKASESISGIPD	60
QY	61	RFGSGSGTDFLTITSSLEPEDPAVYCCQSSGSMPTFGGKVEI	106
DB	61	RFGSGSGTDFLTITSLRLEPEDPAVYCCQSSSMPLTFGGKVEI	106

Search completed: February 13, 2001, 09:03:17
 Job time: 25 sec